

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: November 22, 2000, 00:37:25 ; Search time 1014.24 Seconds
(without alignments)
3608.645 Million cell updates/sec

Title: US-08-955-572-1

Perfect score: 838

Sequence: 1 aatcagcttcttagtatca.....aatagggtgtgggaacttt 838

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1033670 seqs, 2183789903 residues

Total number of hits satisfying chosen parameters: 2067340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl :

1: gb_ba1:*
2: gb_ba2:*
3: gb_om:*
4: gb_ov:*
5: gb_pat:*
6: gb_ph:*
7: gb_pl1:*
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90: gb_htg23:*
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92: gb_sts2:*
93: gb_vl1:*
94: gb_vl2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	836.4	99.8	1415	5	I68025	I68025 Sequence 7
2	836.4	99.8	1415	66	HS003397	U03397 Human recep
3	836.4	99.8	1415	91	G28572	G28572 human STS S
4	833.2	99.4	1419	67	HUMILAX	L12964 Human activ
5	339.2	40.5	2350	12	MUSTC41BB	J04492 Mouse T-cel
6	331.4	39.5	768	5	I68024	I68024 Sequence 5
c	7	144.8	17.3	65	HS892F13	AL009183 Human DNA
	8	144.8	17.3	78	AC025225	AC025225 Homo sapi
c	9	144.8	17.3	78	AC025220	AC025220 Homo sapi
	10	138	16.5	88	AL365441	AL365441 Homo sapi
c	11	134.8	16.1	78	AC025220	AC025220 Homo sapi
	12	120.4	14.4	78	AC025225	AC025225 Homo sapi

13	72.2	8.6	12260	12	MMU02567	U02567	Mus musculus
14	45.6	5.4	7218	5	166494	166494	sequence 14
15	43.2	5.2	179376	76	AC022809	AC022809	Homo sapi
16	42.2	5.0	7218	5	166494	166494	Sequence 14
17	39	4.7	68927	80	AC034302	AC034302	Homo sapi
18	38.2	4.6	156399	8	AC002456	AC002456	Human BAC
19	37	4.4	92128	8	AC003671	AC003671	Arabidops
20	37	4.4	146863	84	AC073392	AC073392	Oryza sat
21	37	4.4	195577	86	AL139816	AL139816	Homo sapi
22	36.8	4.4	12460	12	RN0010709	AJ010709	Rattus no
23	36.8	4.4	179381	81	AC055863	AC055863	Homo sapi
24	36.6	4.4	114771	65	HS569D19	AL022334	Human DNA
25	36.4	4.3	11172	71	AC013030	AC013030	Drosophil
26	36.4	4.3	56820	33	DMB7C10	AL121804	Drosophil
27	36.4	4.3	94585	66	HS047041P4	AL109922	Human DNA
28	36.4	4.3	289090	31	AE003424	AE003424	Drosophil
29	36.2	4.3	174128	89	AP001123	AP001123	Homo sapi
30	36.2	4.3	196292	84	AC073388	AC073388	Mus muscu
31	36	4.3	1784	66	HSFAA03	AF098012	Homo sapi
32	36	4.3	128665	85	AL137799	AL137799	Homo sapi
33	36	4.3	126613	66	HSJ603114	AL122001	Human DNA
34	36	4.3	129536	90	HS080815	AL122015	Homo sapi
35	36	4.3	138781	89	AP002764	AP002764	Homo sapi
36	36	4.3	194399	86	AL157894	AL157894	Homo sapi
37	35.8	4.3	3133	5	IT5000	IT5000	Sequence 1
38	35.8	4.3	3135	4	GCEK6A	T19110	G.gallus Ce
39	35.8	4.3	86224	88	AL360174	AL360174	Homo sapi
40	35.8	4.3	121492	10	AC006976	AC006976	Homo sapi
41	35.6	4.2	82024	77	AC023210	AC023210	Homo sapi
42	35.6	4.2	207585	84	AC073779	AC073779	Mus muscu
43	35.4	4.2	179651	9	AC005553	AC005553	Homo sapi
44	35.2	4.2	1398	66	HSAPQ501	U46566	Human aqp51
45	35.2	4.2	153863	78	AC025361	AC025361	Homo sapi

ALIGNMENTS

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RESULT      1
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LOCUS       1415 bp      DNA
DEFINITION  Sequence 7 from patent US 5674704.
ACCESSION   168025
VERSION     168025.1  GI:2830147
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
             Unclassified.
REFERENCE   1 (bases 1 to 1415)
AUTHORS     Goodwin,R.G., Smith,C.A. and Alderson,M.R.
TITLE       Cytokine designated 4-IBB ligand
JOURNAL     Patent: US 5674704-A 7 07-OCT-1997;
FEATURES    Location/Qualifiers
             source          1..1415
                        /organism="unknown"
BASE COUNT   385 a      332 c      333 g      365 t
ORIGIN
Query Match          99.98;   Score 836.4;   DB 5;   Length 1415;
Best Local Similarity 99.9%;   Pred. No. 1.1e-245;
Matches 837; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY      1 aatcagctttgctagtcataccctgtgccagatttcacatgggaacagctgtttacaa 60
          |||||||
Db       80 AATCAGCTTTGCTAGTATCATACCTGTGCCAGATTTTCATATGGGAACAGCTGTTACAA 139
QY      61 catagtagccactctgttgcctgcctcaactttgagagacagatcattgcaggatcc 120
          |||||||
Db      140 CATAGTAGCCACTCTGTGTGCTGGTCCCTCACTTTGAGAGGCACAGATCATTCAGAGATCC 199
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/organism="Homo sapiens"
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/tissue_type="peripheral blood"
/cell_type="T cell"
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transmembrane protein"
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531..533
misc_feature
/notes="encodes potential glycosylation site"
564..566
misc_feature
/notes="encodes potential glycosylation site"
678..758
misc_feature
/notes="encodes transmembrane domain; amino acids 187-208"
BASE COUNT 385 a 332 c 333 g 365 t
ORIGIN

Query Match 99.8%; Score 836.4; DB 66; Length 1415;
Best Local Similarity 99.9%; Pred. No. 1.1e-245;
Matches 837; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 aatcagtttgtagtatcatatcctggtccagagatttcatctatgagaaacagctgttacaa 60
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DB 80 AATCAGCTTTGCTAGTATCATCTGTCAGGATTTTCATCTGCGAAGAACAGCTGTTCACAA 139
|||||
QY 61 catagtagccactctgttgcgtgcctcaactttgagagagacaagatcattgcaggatcc 120
|||||
DB 140 CATAGTAGCCACCTCTGTTGCTGCTCAACTTTGAGAGGACAAAGATCATTCAGGATCC 199
|||||
QY 121 ttgtagtaactgccagctggtacattctgtgataataacagaatcagatttgcagtc 180
|||||
DB 200 TTGTAGTAAGTCCAGCTGCTGATCTCTGTGATAATAACAGGAATCAGATTTGCAGTCC 259
|||||
QY 181 ctgtctccaaatagtttccagccagctggacaaagacctgtgacatatgcaggca 240
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DB 260 CTGTCTCCAAATAGTTTCTCCAGCGAGGTGGACAAAGACCTGTGACATATGCAGGCA 319
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QY 241 gtgtaaaaggtgtttcaggagaccaggaaggtgttccctccaccagcaatgcagagtga 300
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DB 320 GTGTAAAGGTGTTTTCAGGACCAAGGAAGAGTGTCTCTCCACCAGCAATGCAGAGTGA 379
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QY 301 ctgacatccagggtttcactgcctggtggggcagagatgcagcatgtgtgaacagattgtaa 360
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DB 380 CTGCACTCCAGGGTTTCACTGCCTGGGGCAGGATGCAGCATGTGTGAACAGGATTTGTA 439
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QY 361 acaaggtcaagaactacaaaaaaggttgtaaagactgtgtcttggatggaagctgtgct 420
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DB 440 ACAAGGTCAAGAACTGACAAAAAAGGTTGTAAGACTGTGTCTTTGGGACATTTAACGA 499
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QY 421 tcagaacgtggcatctgtgacccctggacaaactgttcttggatggaagctgtgct 480
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DB 500 TCAGAAACGTGGCATCTGTGACCCCTGGACAAACTGTCTTTGGATGGAAGCTGTGCT 559
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QY 481 tgtgaatggacaagagagagagctgtgtgtgacacatctccagctgacatctctcc 540
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DB 560 TGTGAATGGGACAAAGAGAGAGGAGCTGTGTGTGGACCATCTCCAGCCGACCTCTCTCC 619
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QY 541 ggaagatcctctgtgaccccgctgcccctggagagagaccagacatctctccgagat 600
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DB 620 GGGAGCATCTCTGTGACCCCGCTGCCCCCTGGCAGAGAGCCAGGACACTCTCCGCAGAT 679
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QY 601 catctcctcttctgtcgtgactgcagctgcgtgtgcttctctctctctctccac 660
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Db 680 CATCTCCTTTCTTCTTCTGCGTGACGTCGACTGCTGCTTCTTCTGCTGTTCTTCTTCTCAC 739
QY 661 gctcgtttctctgttttaaacggggcagaaagaaactcctgtatatattcaaacacc 720
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Db 740 GCTCCGTTTCTGTTGTTAAACGGGCGAGAAAGAACTCCTGTATATATTTCAACAACC 799
|||||
QY 721 atttatgagaccagtacaaactactcaagaggaagatggctgtagctgcqatattccaga 780
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Db 800 ATTATGAGACCAGTACAACTACTCAAGAGGAAGATGGCTGTAGCTGCCGATTTCCAGA 859
|||||
QY 781 agaagaagaaggaggtgtgaactgtgaaatggaagtcaatagggctgttgggacttt 838
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Db 860 AGAAGAAGAAGGAGGATGTAACGTGAAATGGAAGTCAATAGGCTGTGTTGGGACTTT 917
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RESULT 3
LOCUS G28572 1415 bp DNA STS
DEFINITION human STS SHGC-35316, sequence tagged site.
ACCESSION G28572
VERSION G28572.1 GI:1408387
KEYWORDS STS; STS sequence; primer; sequence tagged site.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1415)
AUTHORS Myers,R.M.
JOURNAL Unpublished (1996)
COMMENT
Contact: Richard M. Myers
Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford, CA 94305, USA
Tel: 4157259687
Fax: 4157259689
Email: myers@shgc.stanford.edu
Primer A: TGAATGGAGTCAATAGGCG
Primer B: AAAAAGTGGTGCATTTTAAAGG
STS size: 180
PCR Profile:
Initial incubation: 94 degrees C for 90 seconds
Denaturation: 94 degrees C for 15 seconds
Annealing: 62 degrees C for 23 seconds
Polymerization: 72 degrees C for 30 seconds
PCR Cycles: 30
Thermal Cycler: Perkin Elmer 9600
Protocol:
Template: 25 ng
Primer: each 1 uM
dNTPs: each 200 uM
Taq Polymerase: 0.05 units/ul
Total Vol: 10 ul
Buffer:
MgCl2: 2.5 mM
KCl: 50 mM
Tris-HCl: 20 mM
pH: 8.3

```

Prepared with primer pairs provided by Sandoz, derived from U03397
 -- Washington University/Merck EST sequence.

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1..1415
/organism="Homo sapiens"
/map="1"
STS
885..1064
primer_bind
885..905
primer_bind complement(1041..1064)
BASE COUNT 385 a 332 c 333 g 365 t

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Db 280 CTGTCTCTCCAAATAGTTTCTCCAGCGCAGGTGCACAAAGGACCTGTGCACATATGCAGGCA 339
QY 241 gtgtaaagtggttttcaggaccagaagagtggttctccaccagacaatgcagagtgtga 300
Db 340 GTGTAAAGTGTTTTCAGGACCAGGAAGAGTGTCTCTCCACCAGCAATGCAGAGTGTGA 399
QY 301 ctgcactccagggtttcactgcctggggcaggatgcagcatgtggaacagatgttaa 360
Db 400 CTGCACTCCAGGTTTCATCTGCTGGGGCAGGATGCAGCATGTGTGAACAGGATGTAA 459
QY 361 acaaggtcaagaactgacaaaaaaggttgaagactgttgcttgggacatttaacga 420
Db 460 ACAAGGTCAAGAACTGACAAAAAAGGTTGTAAGACTGTGTGTTGGGACATTTAAACGA 519
QY 421 tcagaaactggcatctgtcgaccttgacaaacttcttcttggatggaaagtcctgtct 480
Db 520 TCAGAAACCTGGCATCTGTGACCCCTGGACAAACTGTTCTTTGGATGGAAAGTCTGTGCT 579
QY 481 tgtgaatggagcaagagagagacgtgctctgtgacacatctccagctgacctctctcc 540
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QY 541 gggagcatctctgtgacccccgctcgccctgcgagagagccagacactctccgcagat 600
Db 640 GGGAGCATCTCTGTGACCCCGCTCGCCCTGCGAGAGAGCCAGGACACTCTCCGCAGAT 699
QY 601 catctctcttcttgctgagctgagctgagctgctgtgacacatctccagctgacctctcc 660
Db 700 CATCTCTCTTCTTCTTTCGCTGACGTGACGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 759
QY 661 gctccgttctctgtttaaaggcgagagaaagaaacccctgtatatattcaacaacc 720
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QY 721 attatgagaccagtacaaactactcaagaggagatggctgtgagctgcccagatttccaga 780
Db 820 ATTTATGAGACCAGTACAAACTACTCAAGAGGAAGATGCTGTAGCTGCCGATTTCCAGA 879
QY 781 agaagaagaagagagtgtaactgtgaatggaaatgaatagggctgttggacattt 838
Db 880 AGAAGAAGAAGGAGGATGTGAATGTGTAATGGAAGTCAATAGGGCTGTGTGGACTTT 937

RESULT 5
MUSC41BB
LOCUS
DEFINITION Mouse T-cell receptor 4-1BB protein mRNA, complete cds.
ACCESSION J04492
VERSION J04492.1 GI:201121
KEYWORDS T-cell receptor
SOURCE Mouse (strain C57BL/6) T-lymphocyte cell lines L2 and L3, cDNA to mRNA.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 2350)
AUTHORS Kwon,B.S. and Weissman,S.M.
TITLE cDNA sequences of two inducible T-cell genes
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 86, 1963-1967 (1989)
MEDLINE 8918457
COMMENT Draft entry and clean copy of sequence for [1] kindly provided by B.S.Kwon, 17-MAR-1989.
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            /db_xref="taxon:10090"
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ORIGIN Unreported.

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Best Local Similarity 67.8%; Pred. No. 6.3e-93;
Matches 537; Conservative 0; Mismatches 243; Indels 12; Gaps 4;

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Db 119 AGTGTCTCTGTCATGTGCATTTTCGCCATGGGAAACAACGTGTACAACGGTGGTGCATT 178
QY 74 ctgttgctgtctcaactttgagagagaagatcatctgaggatctcttagtaactgc 133
Db 179 GTGCTGCTGTACTGGCTCTGTGAAGGTGGAGCCGTGCAGAACTCTCTGTGATAACTGT 238
QY 134 ccagctggtacattctgtgataataacaggaatcagatttgagctcctctcccaaat 193
Db 239 CAGCTGTGTACTTCTGCAGAAAATAC---AATCCAGTCTGCAGAGCTGCCCTCCCAAGT 295
QY 194 agttctccagcgagtggaacaaagacctgtgacatatgcagcgagctgtaaaagtgtt 253
Db 296 ACCTTCTCCAGCATAGTGTGGACAGCCGAACTGTGAACATCTGCAGAGTGTGTGCAGCTAT 355
QY 254 tcaggaccaggagagtggttctctccaccagacaatgcagagtgctgactgcactccaggg 313
Db 356 TTCAGGTTCAGAAAGTTTGTCTCTTACCCACAAACCGGAGTGTGATTCATTTGAAGGA 415
QY 314 ttcaactgcctggggcagatgcagcatgtgtgaacagattgtaaacaggttaacaaagtc 373
Db 416 TTCTATTGCTTGGGGCCACAGTGCACCATGTGAAAAGGACTGCAGGCTGCCCGCAGAG 475
QY 374 ctgacaaaaaagttgtaagactgttcttgggacatttgaacatcagacgaacg---t 430
Db 476 CTAACGAAGCAGGGTTGCAAAACCTGTAGCTTGGGAACATTTAATGACCAACGGTACT 535
QY 431 ggcattctgcagccctggacaaactgttcttggatggaaagtctgtgtgtaattggg 490
Db 536 GGGCTCTGTCCGCCCTGGAGCACTGCTCTTAGACGGAAAGGTGTGTCTTAAGACCGGG 595
QY 491 acgaagagagagagcgtgtgtctgtggaccatctccagctgacctctctccgggagatcc 550
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QY 551 tctgtgaccccgctgcctccctgcgagagagccagacactctccgcagatcatctcttc 610
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Db 713 TTCTGTGGCGCTGACATCG---GCTTTGCTGCTGGCCCTGTATCTTCATTACTCTCTCTTC 769
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Db 770 TCTGTGCTCAAAATGGATCAGGAAAAAATCCCCACATATTCAGACCAACCATTTTAAAG 829
QY 731 ccagtaacaaactactcaagaggaagatggctgtagctgcccagattccagagaagaagaa 790
Db 830 ACCACTGGACGACTCAAGAGGAAGATGCTGTAGCTGCCGATGCTCCACAGGAAGAA 889
QY 791 ggagatgtgaa 802
Db 890 GGAGGAGGAGGA 901
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RESULT	6
I68024	I68024
LOCUS	Sequence 5 from patent US 5674704.
DEFINITION	DNA
ACCESSION	I68024
VERSION	I68024.1 GI:2830146
KEYWORDS	Unknown..
SOURCE	Unknown..
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 768)
AUTHORS	Goodwin,R.G., Smith,C.A. and Alderson,M.R.
TITLE	Cytokine designated 4-1BB ligand
JOURNAL	Patent: US 5674704-A 5 07-OCT-1997;
FEATURES	Location/Qualifiers
source	1..768
- BASE COUNT	188 a 186 c 217 g 177 t
- ORIGIN	/organism='unknown'
Query Match	39.5%; Score 331.4; DB 5; Length 768;
Best Local Similarity	68.2%; Pred. No. 1.3e-90;
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QY	101 acaaagtattcgagcatcttgtagtaactgccagctggttacattcttgtataataac 160
Db	61 GTGGGACCGCTGCAGAACTCCTGTGATAACTGTCACTCCCTGGTACCTTCCTGAGAAAATAC 120
QY	161 aggaatcagaattgcagtcacctctcccaaatagtttctccagcgagggtggacaaaagg 220
Db	121 --AATCCAGTCTGCAAGAGCTGCCCTCCAAGTACTCTTCCAGCATAGGTGACAGCGC 177
QY	221 acctgtgacatatgcaggcagtgtaaaagggtgtttccaagaccaggaagagtgctccccc 280
Db	178 AACTGTAAATCTGCAAGAGTGTGCAGCTATTTTCAGGTTCAAAGAGTTTTGCTCCCTCT 237
QY	281 accagcaatgcagagtgtagtgcactccaggtttcactgctcggggcaggatgcagc 340
Db	238 ACCCACAAACGGGAGTGTGAGTGCATTGAAGGATTCATTGCTTGGGGCCACAGTGCACC 297
QY	341 atgtgtgaacagagattgttaacaagagtcgaagactgacaaaaaagggtttaagactgt 400
Db	298 AGATGTGAAGAGACTGCAGGCCTGGCCAGGAGCTAACGAAGCAGGTTGCAAAACCTGT 357
QY	401 tgctttggagacatttaacgatcagaaaacg---tgccatctgtcgacctggacaaactgt 457
Db	358 AGCTTGGGAACAATTTAATGACCAGAACGGTACTGGCGTCTGTCGACCTTGGAGCAACTGC 417
QY	458 tccttggatgaaagtctgtctgttgaatggagcgaagagagacgttgtctgtgga 517
Db	418 TCTCTAGAGGARAGTCTGTGCTTAAGACCGGAGCACCGAAGAGACGTGTGTGTGGA 477
QY	518 ccattctccagctgacctctctccggagagcatcctctgtgacccccgcctgcccctcgaga 577
Db	478 CCCCTGTGTGAGCTTCTCTCCAG---TACCACCATTTCTGTGACTCCAGAGGGAGGA 534
QY	578 gagcaggacacatctccgagatcatcctctcttttttctgtgctgacgtcgactcggttg 637
Db	535 CCAGGAGGGACATTCCTTGCAAGTCTTACCTTGTTCCTGGCCCTGACATCG---GCTTTG 591
QY	638 ctcttctcgtgttcttctcactccgctttctctctgttgttaaagggggcagaagaaa 697
Db	592 CTGCTGCCCTGATCTTCATTACTCTCCTGTCTCTGTGCTCAATGGATCAGGAAAAA 651
QY	698 ctctgttatatatcaaacacacatttatgagaccagttacaactactctaagaggaagat 757
Db	652 TTCCCCCACAATTTCAAGAACCACTTTAAGAGAGACACCTTGGAGCAGCTCAAGAGGAAGAT 711

Qy	758	ggcgtgactgccgattccagaagaagaagaggaggtgaa	802
Db	712	GCTTGTAGCTCCGATGTCCACAGGAAGAGAGGAGGAGGA	756
RESULT	7		
HS892F13/c			
LOCUS	HS892F13	65848 bp	DNA
DEFINITION	Human DNA sequence from clone 892F13 on chromosome 1p36.2-36.3		PRI
	Contains the gene for TNFRSF9 (tumor necrosis factor receptor		
	superfamily, member 9), ESTs, STSs, and GSSs, complete sequence.		
ACCESSION	AL009183		
VERSION	AL009183.10	GI:5679755	
KEYWORDS	HTG; TNFRSF9;		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;		
AUTHORS	Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	1 (bases 1 to 65848)		
JOURNAL	Direct Submission		
	Submitted (04-OCT-1999) Sanger Centre, Hinxton, Cambridgeshire,		
	CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk		
COMMENT	requests: clonerequest@sanger.ac.uk		
	On Aug 3, 1999 this sequence version replaced gi:550608.		
	During sequence assembly data is compared from overlapping clones.		
	Where differences are found these are annotated as variations		
	together with a note of the overlapping clone name. Note that the		
	variation annotation may not be found in the sequence submission		
	corresponding to the overlapping clone, as we submit sequences with		
	only a small overlap as described above.		
	This sequence has been finished according to sequence map criteria		
	as follows. An attempt is made to resolve all sequencing problems,		
	such as compressions and repeats, but not necessarily within known		
	annotated human repeat sequence elements (e.g. Alu). Where the		
	sequence is ambiguous, there is an annotation using the 'unsure'		
	feature key.		
	This sequence was generated from part of bacterial clone contigs of		
	human chromosome 1, constructed by the Sanger Centre Chromosome 1		
	Mapping Group. Further information can be found at		
	http://www.sanger.ac.uk/HGP/Chr1		
	892F13 is from the library RPCI-5 constructed at the Roswell Park		
	Cancer Institute by the group of Pieter de Jong. For further		
	details see http://bacpac.med.buffalo.edu/ VECTOR: pcYAC2 The		
	following abbreviations are used to associate primary accession		
	numbers given in the feature table with their source databases:		
	Em.; EMBL; Sw.; SWISSPROT; Tr.; TREMBL; Wp.; WORMPEP; Information		
	on the WORMPEP database can be found at		
	http://www.sanger.ac.uk/Projects/C_elegans/wormpep IMPORTANT: This		
	sequence is not the entire insert of clone 892F13. It may be		
	shorter because we only sequence overlapping sections once, or		
	longer because we arrange for a small overlap between neighbouring		
	submissions.		
	The true left end of clone 215D11 is at 14471 in this sequence. The		
	true right end of clone d3467L1 is at 100 in this sequence.		
FEATURES	Location/Qualifiers		
source	1..65848		
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	/db_xref="taxon:9606"		
	/chromosome="1"		
	/map="p36.2-36.3"		
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	/clone="RP5-892F13"		
	168..525		
repeat_region	/note="179 copies 2 mer gg 54% conserved"		
misc_feature	435..533		
	/note="Weak data"		
repeat_region	1363..1662		
	/note="Alusg repeat: matches 1..310 of consensus"		
repeat_region	2081..2370		
	/note="AluJb repeat: matches 12..305 of consensus"		
repeat_region	3452..3639		

repeat_region	15407. .15757 /note="L1M4 repeat: matches 3340. .3690 of consensus"
repeat_region	15781. .16029 /note="L2 repeat: matches 1847. .2113 of consensus"
repeat_region	16060. .16113 /note="M1R repeat: matches 196. .250 of consensus"
repeat_region	16126. .16159 /note="17 copies 2 mer ta 82% conserved"
repeat_region	16167. .16222 /note="28 copies 2 mer tg 71% conserved"
repeat_region	16225. .16310 /note="M1R repeat: matches 120. .204 of consensus"
repeat_region	16382. .16481 /note="L2 repeat: matches 1694. .1797 of consensus"
repeat_region	16466. .16621 /note="L2 repeat: matches 2260. .2417 of consensus"
repeat_region	17192. .17311 /note="AluJ repeat: matches 2. .126 of consensus"
repeat_region	17580. .17953 /note="187 copies 2 mer cc 60% conserved"
repeat_region	17625. .17954 /note="110 copies 3 mer cct 78% conserved"
repeat_region	17986. .18280 /note="AluSg repeat: matches 1. .293 of consensus"
repeat_region	18808. .19092 /note="AluJo repeat: matches 34. .306 of consensus"
repeat_region	19215. .19517 /note="AluSx repeat: matches 1. .304 of consensus"
repeat_region	19617. .19728 /note="MLR2FB repeat: matches 1. .119 of consensus"
repeat_region	19729. .20034 /note="AluSg repeat: matches 1. .308 of consensus"
repeat_region	20035. .20048 /note="MLR2FB repeat: matches 119. .132 of consensus"
repeat_region	20049. .20127 /note="MADE1 repeat: matches 1. .80 of consensus"
repeat_region	20128. .20297 /note="MLR2FB repeat: matches 132. .279 of consensus"
misc_feature	complement(20298. .20609)
misc_feature	20298. .20547 /note="match: GSS: Em:AQ425759"
repeat_region	20993. .21102 /note="55 copies 2 mer aa 75% conserved"
repeat_region	21561. .21859 /note="AluSx repeat: matches 1. .299 of consensus"
repeat_region	21958. .22249 /note="AluJo repeat: matches 2. .299 of consensus"
repeat_region	22472. .22611 /note="AluSg repeat: matches 1. .142 of consensus"
repeat_region	22612. .22907 /note="AluSx repeat: matches 1. .301 of consensus"
repeat_region	22908. .23072 /note="AluSg repeat: matches 142. .300 of consensus"
repeat_region	23255. .23400 /note="THE1B repeat: matches 219. .364 of consensus"
repeat_region	23401. .23682 /note="AluSc repeat: matches 1. .295 of consensus"
repeat_region	23683. .23823 /note="THE1B repeat: matches 1. .220 of consensus"
repeat_region	23868. .24164 /note="AluSx repeat: matches 14. .308 of consensus"

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	Best Local Similarity	95.5%;	Pred. No. 5.6e-33;		
	Matches 149; Conservative	0;	Mismatches 7;	Indels 0;	Gaps 0;
Qy	233 tgcaggcagtgtaaaagtgttttcgagaccacgggaaggagtgttctccaccagcaatgcc	292			
Dd	52938 TGGGCGGACTTGTAGTGTTTCAGACACCAGGAAGAGTGTCTCCACCAATGCCA	52879			
Qy	293 gagtgtgactgcacctcccaggatttcactgccctggggcgagcatgtagcatgtggaacag	352			

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR
 Web site: <http://www-seq.wi.mit.edu>
 Contact: sequence_submissions@genome.wi.mit.edu
 ----- Project Information -----
 Center project name: L8035
 Center clone name: 281_E22
 ----- Summary Statistics -----
 Sequencing vector: M13; M77815; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.960731
 Consensus quality: 182912 bases at least Q40
 Consensus quality: 192383 bases at least Q30
 Consensus quality: 195712 bases at least Q20
 Insert size: 217000; agarose-fp
 Insert size: 199373; sum-of-contigs
 Quality coverage: 3.5 in Q20 bases; agarose-fp
 Quality coverage: 3.8 in Q20 bases; sum-of-contigs

 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 35 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.
 *
 * 1 1182: contig of 1182 bp in length
 * 1183 1282: gap of 100 bp
 * 1283 2698: contig of 1416 bp in length
 * 2699 2798: gap of 100 bp
 * 2799 4194: contig of 1396 bp in length
 * 4195 4294: gap of 100 bp
 * 4295 5704: contig of 1410 bp in length
 * 5705 5804: gap of 100 bp
 * 5805 8389: contig of 2585 bp in length
 * 8390 8489: gap of 100 bp
 * 8490 10352: contig of 1863 bp in length
 * 10353 10452: gap of 100 bp
 * 10453 13024: contig of 2572 bp in length
 * 13025 13124: gap of 100 bp
 * 13125 15709: contig of 2585 bp in length
 * 15710 15809: gap of 100 bp
 * 15810 17470: contig of 1661 bp in length
 * 17471 17570: gap of 100 bp
 * 17571 20131: contig of 2581 bp in length
 * 20132 20251: gap of 100 bp
 * 20252 22870: contig of 2619 bp in length
 * 22871 22970: gap of 100 bp
 * 22971 25709: contig of 2739 bp in length
 * 25710 25809: gap of 100 bp
 * 25810 28338: contig of 2529 bp in length
 * 28339 28438: gap of 100 bp
 * 28439 32476: contig of 4038 bp in length
 * 32477 32576: gap of 100 bp
 * 32577 37518: contig of 4942 bp in length
 * 37519 37618: gap of 100 bp
 * 37619 41724: contig of 4106 bp in length
 * 41725 41824: gap of 100 bp
 * 41825 46408: contig of 4584 bp in length
 * 46409 46508: gap of 100 bp
 * 46509 51711: contig of 5203 bp in length
 * 51712 51811: gap of 100 bp
 * 51812 56860: contig of 5049 bp in length
 * 56861 56960: gap of 100 bp
 * 56961 62871: contig of 5911 bp in length
 * 62872 62971: gap of 100 bp
 * 62972 69111: contig of 6140 bp in length
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 * 69212 75632: contig of 6421 bp in length
 * 75633 75732: gap of 100 bp
 * 75733 81565: contig of 5833 bp in length
 * 81566 81665: gap of 100 bp
 * 81666 88181: contig of 6516 bp in length

* 88182 88281: gap of 100 bp
 * 88282 95593: contig of 7312 bp in length
 * 95594 95693: gap of 100 bp
 * 95694 103809: contig of 8116 bp in length
 * 103810 103909: gap of 100 bp
 * 103910 112398: contig of 8489 bp in length
 * 112399 112498: gap of 100 bp
 * 112499 120033: contig of 7535 bp in length
 * 120034 120133: gap of 100 bp
 * 120134 129004: contig of 8871 bp in length
 * 129005 129104: gap of 100 bp
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 * 137575 137674: gap of 100 bp
 * 137675 146983: contig of 9309 bp in length
 * 146984 147083: gap of 100 bp
 * 147084 156907: contig of 9824 bp in length
 * 156908 157007: gap of 100 bp
 * 157008 168350: contig of 11343 bp in length
 * 168351 168450: gap of 100 bp
 * 168451 185212: contig of 16762 bp in length
 * 185213 185312: gap of 100 bp
 * 185313 202773: contig of 17461 bp in length.
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 * /db_xref="taxon:9606"
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 * 13125. .15709
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 * 51812. .56860
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 * 56961. .62871
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 * 62972. .69111
 * /note="assembly_fragment"
 * 69212. .75632

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misc_feature 143744..162975
/note="assembly_name:Contig36"
BASE COUNT 45139 a 35640 c 35357 g 44193 t 2646 others
ORIGIN

Query Match 14.4%; Score 120.4; DB 78; Length 162975;
Best Local Similarity 92.0%; Pred. No. 2e-25;
Matches 127; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
QY 701 ctgtatattcaaacacatttatagaccagatcaactactcaaggaagatggc 760
Db 119307 CTTAAATTTTTTTTTTATGACCTTTATGACCACTACTCAAGAGAGATGGC 119248
QY 761 tgtagctgccattccagaagaagaagagagatgtgaactgtgaagtcaa 820
Db 119247 TGAGCTGCCGATTTTCAGAGAGAGAGAGAGAGAGATGTGACCTGTGAATGGAAGTCAA 119188
QY 821 taggctgttgggacttt 838
Db 119187 TAGGCTGTGGGACTTT 119170
RESULT 13
MMU02567 12260 bp DNA ROD 30-MAR-1996
LOCUS Mus musculus BALB/c T-cell antigen 4-1BB gene, complete cds.

U02567
U02567.1 GI:1117783
mouse.
ORGANISM Mus musculus
REFERENCE 1 (sites) Kwon,B.S., Kozak,C.A., Kim,K.K. and Pickard,R.T.
AUTHORS Genomic organization and chromosomal localization of the T-cell
TITLE antigen 4-1BB
J. Immunol. 152 (5), 2256-2262 (1994)
JOURNAL 94179805
MEDLINE 2 (bases 1 to 12260)
REFERENCE Kwon,B.S.
AUTHORS Direct Submission
TITLE Submitted (18-OCT-1993) Kwon B.S., Indiana University School of
JOURNAL Medicine, Microbiology and Immunology, 635 Barnhill Dr.,
Indianapolis, IN 46202, USA
COMMENT On Dec 14, 1995 this sequence version replaced gi:409177.
FEATURES
source location/Qualifiers
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/organism="Mus musculus"
/strain="BALB/c"
/db_xref="taxon:10090"
/clone="P4-1BB"
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/germline
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9350..9404,9423..9495,10497..10628,11380..11477)
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PVVSPSTTISVTPEGGPGHSLQVLTFLTSLALLALIFITLFLSVLKWIRKRF
PHFKQPFKKTGAQEDACSCRCPOEERGGGGYEL"
BASE COUNT 3262 a 2773 c 2843 g 3382 t
ORIGIN
Query Match 8.6%; Score 72.2; DB 12; Length 12260;
Best Local Similarity 66.2%; Pred. No. 8.6e-11;
Matches 104; Conservative 0; Mismatches 53; Indels 0; Gaps 0;
QY 234 gcaggcagtgtaaagggtttttcaggaccaggaaggagtggtctccaccagcaatgcag 293
Db 7487 GCTGGGCTTTGTAGGCTATTTCAAGTTCAGAGAGTTTGTCTCTTACCCACACGCG 7546
QY 294 agtgctgactccagggtttcactgcctggggcaggatgcagatgtgtaacagg 353
Db 7547 AGTGAGTGCATTGAGGATTCATTGCTTGGGGCCACACGTGCCACCATGTGAAAAGG 7606
QY 354 attgtaacaagggtcagaactgacaaaaaggttg 390
Db 7607 ACTGCGCCCTGGCCAGGAGCTAACGAAGCAGGCTAG 7643
RESULT 14
I66494
LOCUS I66494 7218 bp DNA PAT 28-DEC-1997
DEFINITION Sequence 14 from patent US 5670367.
ACCESSION I66494
VERSION I66494.1 GI:2724471
KEYWORDS Unknown.
SOURCE Unclassified.
ORGANISM
REFERENCE 1 (bases 1 to 7218)

Result No.	Score	Query Match	Length	DB	ID	Description
1	838	100.0	838	16	086126	H4-1BB receptor protein
2	836.4	99.8	838	17	T39546	Human receptor H4
3	836.4	99.8	1415	16	075474	Human 4-1BB polypeptide
4	836.4	99.8	1415	18	T91026	Human 4-1BB receptor
5	836.4	99.8	1439	20	Z09796	Human CD137 cDNA.
6	831.6	99.2	838	20	Z08961	Human receptor protein
7	828.4	98.9	1439	16	092086	Human receptor protein
8	808.8	72.6	946	18	T88999	DNA encoding a human
9	608.8	72.6	946	20	X02162	Human h4-1BBSV receptor
10	339.2	40.5	2347	17	T39541	Mouse receptor protein
11	337.6	40.3	2350	16	086127	4-1BB receptor protein
12	337.6	40.3	2350	20	X30763	Mouse receptor protein

	13	331.4	39.5	768	16	075428	Muscle 4-1BB polyP
	14	331.4	39.5	768	16	T91027	Mouse 4-1BB recept
	15	36.4	4.3	2781	19	V62457	Human dendritic ceel
	16	36.4	4.3	2833	20	X03846	Human tumour necro
	17	35.8	4.3	3133	16	O90652	Eph-related tyrosin
	18	34.8	4.2	1391	19	V41375	RANK partial polyP
	19	34.8	4.2	1391	19	V41369	RANK partial polyP
	20	34.8	4.2	3115	19	V41374	RANK partial polyP
	21	34.8	4.2	3115	19	V41368	RANK partial polyP
	22	34.8	4.2	3136	19	V41376	NF-kB receptor act
	23	34.8	4.2	3136	19	Z36257	NF-kB receptor act
	24	34.8	4.2	3137	21	Z36257	CDNA encoding a hu
	25	34.8	4.2	3602	12	O12849	A. niger pyruvate k
	26	34.2	4.1	10732	21	A10594	Gene encoding a sw
	27	33.8	4.0	38186	20	Z32028	Human MERTH relate
	28	32	3.8	723	19	V19154	Truncated human JI
C	29	31.6	3.8	5059	20	X84332	Stealth virus nucle
C	30	31.6	3.8	15747	20	X13018	Enterococcus faeca
C	31	31.4	3.7	590	11	O06353	Exon 2 of ovine lea
C	32	31.4	3.7	2161	20	X03034	Human IL-1ra BAC c
C	33	31.4	3.7	11901	20	X02958	Human IL-1ra BAC c
C	34	31.2	3.7	2817	19	V57556	Rat Hrs-2 polypept
C	35	31.2	3.7	7156	19	V15586	Lactobacillus bulg
C	36	31	3.7	2271	21	A37108	Human PRO1604 (UNQ
C	37	31	3.7	4067	15	O63192	Human adeno-associ
C	38	31	3.7	235033	19	V57926	Hereditary haemoch
C	39	31	3.7	237326	19	V57903	Hereditary haemoch
C	40	30.8	3.7	2770	20	V87196	EST clone BN171.
C	41	30.6	3.7	291	13	O22192	Tetranucleotide re
C	42	30.6	3.7	291	13	O32787	Microsatellite rep
C	43	30.6	3.7	291	15	O57810	Repeat polymorphis
C	44	30.6	3.7	291	19	V15526	Polyomorphic regio
C	45	30.6	3.7	847	20	Z33450	Human prostate can

ALIGNMENTS

RESULT	1	
ID	Q86126	standard; cdna; 838 BP.
XX	Q86126;	
XX	AC	
XX	DT	16-OCT-1995 (first entry)
XX	DE	H4-1BB receptor protein cdna.
KM	H4-1BB; receptor protein; immunosuppressive; autoimmune disease;	
KW	organ transplantation; cell membrane ligand; ss.	
XX	OS	Homo sapiens.
XX	FH	Key
FT	CDS	Location/Qualifiers
XX		/tag= a
PN	WO9507984-A.	
PD	23-MAR-1995.	
PF	15-SEP-1994;	94WO-US10457.
PR	16-SEP-1993;	93US-O122796.
PA	(INDV) UNIV INDIANA FOUND.	
PI	Kwon BS;	
DR	WI: 1995-131352/17.	
DR	P-PSDB: R70977.	
TX	Novel CDNA encoding human receptor protein H4-1BB - useful to	

PT produce the protein which is used to treat auto-immune disease
 PT and facilitate organ transplantation

PS Claim 2; Fig.2; 36pp; English.

XX Human peripheral blood lymphocyte-derived cDNA was amplified by PCR
 CC using probes based on the mouse receptor protein 4-1BB gene. The PCR
 CC product was used to screen a cDNA library of activated human T-cells.
 CC The isolated cDNA (Q86126), deposited as NRRL B21131, encoded the
 CC human homolog, H4-1BB (R70977), of 4-1BB.

XX Sequence 838 BP; 218 A; 191 C; 215 G; 214 T; 0 other;

Query Match 100.0%; Score 838; DB 16; Length 838;

Best Local Similarity 100.0%; Pred. No. 2, 6e-262;

Matches 838; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 aatcagcttctgtatcatcacctgtgcccagattcatcatgaggaacagctgttaca 60
 Db 1 aatcagcttctgtatcatcacctgtgcccagattcatcatgaggaacagctgttaca 60
 QY 61 catagtagccactctgtgtcgtgcctcaactttgagaggaagatattgagagatcc 120
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 Db 121 ttgtagtaactgcccagctgtgtacattctgtgataataacaggaatcagatttcagctcc 180
 QY 181 ctgtctcccaaatagttctccagcgaggtgacaagaagacctgtgacataatgacagca 240
 Db 181 ctgtctcccaaatagttctccagcgaggtgacaagaagacctgtgacataatgacagca 240
 QY 241 gtgtgaagggtgtttccaggagcaaggaggtgttcccccacagcaatgacaggtgtga 300
 Db 241 gtgtgaagggtgtttccaggagcaaggaggtgttcccccacagcaatgacaggtgtga 300
 QY 301 ctgacaccaggggtttcactgctcgtgggacagatgacagatgacagatgacagatgac 360
 Db 301 ctgacaccaggggtttcactgctcgtgggacagatgacagatgacagatgacagatgac 360
 QY 361 acaaggtcacaagaactgacaaaagaagtgtgaagaactgtgtcttgggacatttaacga 420
 Db 361 acaaggtcacaagaactgacaaaagaagtgtgaagaactgtgtcttgggacatttaacga 420
 QY 421 tcaagaacgtgtgcatctgtgcaccccttgacaaactgttcttggatggaagaagctgtgct 480
 Db 421 tcaagaacgtgtgcatctgtgcaccccttgacaaactgttcttggatggaagaagctgtgct 480
 QY 481 tgtgaatgggacgaaggagagagagctgtgtgacacatccacagctgacccctccccc 540
 Db 481 tgtgaatgggacgaaggagagagagctgtgtgacacatccacagctgacccctccccc 540
 QY 541 gggagacatctctgtgaccccgctgcgcctcgagagagccagagacatctccgcagat 600
 Db 541 gggagacatctctgtgaccccgctgcgcctcgagagagccagagacatctccgcagat 600
 QY 601 catctctcttcttctgtgcgtgacgtgcagctgtgtcttctctgctgcttcttccctaac 660
 Db 601 catctctcttcttctgtgcgtgacgtgcagctgtgtcttctctgctgcttcttccctaac 660
 QY 661 gctccgcttctctgtgtttaaagcgagcaagaagaactcctgtatataatcaacaacc 720
 Db 661 gctccgcttctctgtgtttaaagcgagcaagaagaactcctgtatataatcaacaacc 720
 QY 721 attatagaaccagttacaactactcaagaggaagatggtgtgactgctgcgattccaga 780
 Db 721 attatagaaccagttacaactactcaagaggaagatggtgtgactgctgcgattccaga 780
 QY 781 agagaagaaggagagatgtgaactgtgaatgaatgaatgaatgaatgaatgaatgaatga 838
 Db 781 agagaagaaggagagatgtgaactgtgaatgaatgaatgaatgaatgaatgaatgaatga 838

RESULT 2

ID T39546 standard; cDNA to mRNA; 838 BP.

AC T39546;

DT 12-DEC-1996 (first entry)

XX Human receptor H4-1BB cDNA.

KW Receptor 4-1BB; H4-1BB; monoclonal antibody; T-lymphocyte; T-cell;
 KW immunostimulant; cancer; autoimmune disease; graft rejection;
 KW therapy; ss.

OS Homo sapiens.

XX Key Location/Qualifiers

FT CDS 41..808

FT mat_peptide 41..805

FT /*tag- a

FT /*tag- b

PN WO9629348-A1.

PD 26-SEP-1996.

PF 22-MAR-1996; 96WO-US03965.

PR 23-MAR-1995; 95US-0409851.

XX (INDV) UNIV INDIANA FOUND.

PA Kang C, Kwon BS;

PI WPI; 1996-443138/44.

XX P-PSDB; W04174.

DR Monoclonal antibody specific for human receptor protein 4-1BB - used

PT to enhance proliferation and activation of T-cells for treatment of

PT cancer and to inhibit specific ligand binding for treating

PT auto-immune diseases

PS Disclosure; Page 36-37; 48pp; English.

XX A cDNA clone (T39546) codes for novel human receptor protein

CC H4-1BB (W04174), a protein that has the potential to function as

CC an accessory signaling molecule during T-cell activation and

CC proliferation. The cDNA clone was isolated from a lambda gt11

CC cDNA library of activated human T lymphocytes by screening with a

CC PCR product obd. by amplification of lymphocyte cDNA using

CC primers (see also T39542-45) based on the murine 4-1BB cDNA

CC (T39541). It can be used to produce recombinant H4-1BB useful

CC for isolating H4-1BB ligands, for stimulating proliferation of

CC B-cells expressing H4-1BB ligands, for blocking H4-1BB ligand

CC binding and for raising anti-H4-1BB monoclonal antibody.

XX Sequence 838 BP; 218 A; 192 C; 214 G; 214 T; 0 other;

Query Match 99.8%; Score 836.4; DB 17; Length 838;

Best Local Similarity 99.9%; Pred. No. 8, 8e-262;

Matches 837; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 aatcagcttctgtatcatcacctgtgcccagattcatcatgaggaacagctgttaca 60
 Db 1 aatcagcttctgtatcatcacctgtgcccagattcatcatgaggaacagctgttaca 60
 QY 61 catagtagccactctgtgtcgtgcctcaactttgagaggaagatattgagagatcc 120
 Db 61 catagtagccactctgtgtcgtgcctcaactttgagaggaagatattgagagatcc 120

```
QY 121 ttgtaagtaactgccagctgtacattctgtgataataacagaagatctgcagctcc 180
    |||
Db 121 ttgtatgaactgcgcagctgtgtacattctgtgataataacagaagatctgcagctcc 180
QY 181 ctgtccctccaaatagtcttcacagcgaggctgacaaaggacgtgtacatatgacgca 240
    |||
Db 181 ctgtccctccaaatagtcttcacagcgaggctgacaaaggacgtgtacatatgacgca 240
QY 241 gttttaaagggttcttcagagccaggaaggagtgttccctccacagcaatcagaagtga 300
    |||
Db 241 gttttaaagggttcttcagagccaggaaggagtgttccctccacagcaatcagaagtga 300
QY 301 ctgcacactccagaggtttcaacgacctgggggagcagagatgtgtataaaggatttaa 360
    |||
Db 301 ctgcacactccagaggtttcaacgacctgggggagcagagatgtgtataaaggatttaa 360
QY 361 acaaggctcaagaactgacaaataaaggctgtlaaagaactgtgtcttggagcatltaacga 420
    |||
Db 361 acaaggctcaagaactgacaaataaaggctgtlaaagaactgtgtcttggagcatltaacga 420
QY 421 tcagaaacgttgcatactgttcgacccctgagacaactgttcttggatggaaagtctgtct 480
    |||
Db 421 tcagaaacgttgcatactgttcgacccctgagacaactgttcttggatggaaagtctgtct 480
QY 481 tgtgaatggagcagaaggagagagcgtgtctgttgagccatctccagctcacctctcc 540
    |||
Db 481 tgtgaatggagcagaaggagagagcgtgtctgttgagccatctccagctcacctctcc 540
QY 541 gggagacatctctgtgaccccgctgcctctgcagagagccaggaacactccgcagat 600
    |||
Db 541 gggagacatctctgtgaccccgctgcctctgcagagagccaggaacactccgcagat 600
QY 601 catctccctctctctgtgcgtgcgtgcagctgcagctgcgtctctctctctctccac 660
    |||
Db 601 catctccctctctctgtgcgtgcgtgcagctgcagctgcgtctctctctctccac 660
QY 661 gtcctccttctctgtgttataacggggcagaagaactcctgtatatataacaaacc 720
    |||
Db 661 gtcctccttctctgtgttataacggggcagaagaactcctgtatatataacaaacc 720
QY 721 atttaatgagaccagtaacaaactactcaagaggaagatgtgtgtagctgcgcatltaacga 780
    |||
Db 721 atttaatgagaccagtaacaaactactcaagaggaagatgtgtgtagctgcgcatltaacga 780
QY 781 agaagaagaaggagatgtgtgaactgtgaaatggaagtaacatagagctgtgtggaactt 838
    |||
Db 781 agaagaagaaggagatgtgtgaactgtgaaatggaagtaacatagagctgtgtggaactt 838

RESULT 3
Q75424
ID Q75424 standard; cDNA to mRNA; 1415 BP.
AC Q75424;
XX
XX 08-AUG-1995 (first entry)
DT
XX
XX Human 4-1BB polypeptide coding sequence.
DE
XX
XX T-cell: lymphocyte: activation; tissue culture; clone; cell lines;
KM proliferation; stimulation; 4-1BB-L; ligand; receptor; cytokine; ss.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH CDS 120..887
FT /*tag= a
FT /product= 4-1BB polypeptide.
FT sig_peptide 120..188
FT /*tag= b
FT mat_peptide 189..884
FT /*tag= c
XX
```

```
PN W09426290-A.
XX
XX 24-NOV-1994.
PD
XX
XX 06-MAY-1994; 94MO-US05036.
PF
XX
XX 07-MAY-1993; 93US-0060843.
PR
XX
XX (IMMUNEX CORP.
PA
XX
XX Alderson MR, Goodwin RG, Smith CA;
PI
XX
XX WPI: 1995-022265/03.
DR
XX
XX P-PSDB; R64197.
PT
XX
XX Cytokine, 4-1BB ligand (4-1BB-L) - binds to cell surface receptor
PS Claim 29; Page 46-47; 65pp; English.
XX
XX The 4-1BB polypeptide (receptor) and the 4-1BB-L (cytokine, see
CC Q75423) are useful in a pharmaceutical composition for stimulating
CC the immune system. The 4-1BB and 4-1BB-L polypeptides are also useful
CC for exploring mechanisms of T-cell activation, as they are expressed
CC on T lymphocytes. 4-1BB-L can be used as a tissue culture reagent for
CC in vitro cultivation of primary T-cells during the derivation of
CC clonal T-cell lines. It may also be used to stimulate proliferation
CC of activated T-cells, used in therapeutic procedures.
XX
XX Sequence 1415 BP; 385 A; 332 C; 333 G; 365 T; 0 other;
```

```
Query Match 99.8%; Score 836.4; DB 16; Length 1415;
Best Local Similarity 99.9%; Pred. No. 1.2e-261;
Matches 837; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 aatgaagtttgctatgatatcaactgtgcccagattcattatgggaaacagctgttaaa 60
    |||
Db 80 aatgaagtttgctatgatatcaactgtgcccagattcattatgggaaacagctgttaaa 139
QY 61 catatgagccactgtgtgtgtgtcctcaacttttgagagaggaagatattgcagagatcc 120
    |||
Db 140 catatgagccactgtgtgtgtgtcctcaacttttgagagaggaagatattgcagagatcc 199
QY 121 ttgtagtaactgcgcagctgtgtacattctgtgataataacagaagatctgcagctcc 180
    |||
Db 200 ttgtagtaactgcgcagctgtgtacattctgtgataataacagaagatctgcagctcc 259
QY 241 gttgtaaaagggttcttcagagccaggaaggagtgttccctccacagcaatgaaagtga 300
    |||
Db 320 gttgtaaaagggttcttcagagccaggaaggagtgttccctccacagcaatgaaagtga 379
QY 301 ctgcacactccagaggtttcaactgcctcctggggcagagatgcagcatgtgtgaacggattgaa 360
    |||
Db 380 ctgcacactccagaggtttcaactgcctcctggggcagagatgcagcatgtgtgaacggattgaa 439
QY 361 acaaggctcaagaactgacaaataaaggctgtlaaagaactgtgtcttggagcatltaacga 420
    |||
Db 440 acaaggctcaagaactgacaaataaaggctgtlaaagaactgtgtcttggagcatltaacga 499
QY 421 tcagaaacgttgcatactgttcgacccctgagacaactgttcttggatggaaagtctgtct 480
    |||
Db 500 tcagaaacgttgcatactgttcgacccctgagacaactgttcttggatggaaagtctgtct 559
QY 481 tgtgaatggagcagaaggagagagcgtgtctgttgagccatctccagctcacctctcc 540
    |||
Db 560 tgtgaatggagcagaaggagagagcgtgtctgttgagccatctccagctcacctctcc 619
QY 541 gggagacatctctgtgaccccgctgcctctgcagagagagcaggaacactccgcagat 600
```

```

|||||
Db 620 ggagacacccctctgaccccgccgacgagagacgacacaccccgagat 679
QY 601 catccctctctctgctgacgacgacgacgacgacgacgacgacgacgac 660
Db 680 catctctctctctctgctgacgacgacgacgacgacgacgacgacgacgac 739
QY 661 gtcctgtctctctgtgttaaacgggagagaaactcgtatataatcaaac 720
Db 740 gtcctgtctctctgtgttaaacgggagagaaactcgtatataatcaaac 799
QY 721 attatgagaccagtaacaaactactcaagagagagatgctgtacgacgattccaga 780
Db 800 attatgagaccagtaacaaactactcaagagagagatgctgtacgacgattccaga 859
QY 781 agaaagaagaagagatgtgactgtgaactgtgaactgaaggcgtgttgagactt 838
Db 860 agaaagaagaagagatgtgactgtgaactgtgaactgaaggcgtgttgagactt 917

RESULT 4
T91026
ID T91026 standard; cDNA to mRNA, 1415 BP.
XX
AC T91026;
XX
DT 25-FEB-1998 (first entry)
XX
DE Human 4-1BB receptor cDNA clone hu4-1BB.
XX
KW 4-1BB ligand; 4-1BB-L; receptor; human; cytokine; T lymphocyte;
KM T cell; proliferation; immunostimulant; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 120..887
FT FT /*tag= a
FT sig_peptide 120..188
FT FT /*tag= b
FT mat_peptide 189..884
FT FT /*tag= c
XX
XX US5674704-A.
XX
XX PD 07-OCT-1997.
XX
XX PF 07-MAY-1993; 93US-0060843.
XX
XX PR 06-MAY-1994; 94US-0236918.
XX PR 07-MAY-1993; 93US-0060843.
XX
XX PA (IMMV ) IMMUNEX CORP.
XX
XX PI Alderson MR, Goodwin RG, Smith CA;
XX
XX DR WPI: 1997-502333/46.
XX
XX DR P-PSDB; W26658.
XX
XX PT DNA encoding 4-1BB ligand polypeptide(s) - useful for stimulating
XX T-cell proliferation in vitro, and as research tools
XX
XX XX Example 2; Column 43-46; 32pp: English.
XX
XX This cDNA clone encodes human 4-1BB (see W26658), a member of the
XX tumour necrosis factor receptor superfamily that is expressed on
XX cells that include, but are not limited to, stimulated human
XX peripheral blood lymphocytes. The clone was isolated from a cDNA
XX library prepared from human peripheral blood T-lymphocytes that
XX had been activated with phytohemagglutinin and phorbol myristate
XX acetate. A fragment of murine 4-1BB DNA (see T91027) was used
XX as probe. A novel claimed cytokine, designated 4-1BB ligand
XX (4-1BB-L) has been identified, cloned and sequenced (see W26657)

```

CC that binds to 4-1BB. 4-1BB-L, especially its soluble extracellular
 CC domain, can be used to stimulate T-cell proliferation in vitro, as
 CC a research tool and as an affinity ligand for purifying 4-1BB.
 XX
 SQ Sequence 1415 BP; 385 A; 332 C; 333 G; 365 T; 0 other;

Query Match 99.8%; Score 836.4; DB 18; Length 1415;
 Best Local Similarity 99.9%; Pred. No. 1.2e-261;
 Matches 837; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 1 aatcagcttctgtatcatcatcctgtgcagattcatcatatggaagaacgtgttaaca 60
Db 80 aatcagcttctgtatcatcatcctgtgcagattcatcatatggaagaacgtgttaaca 139
QY 61 catatgacccactcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 120
Db 140 catatgacccactcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 199
QY 121 ttgtatgactgcccagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 180
Db 200 ttgtatgactgcccagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 259
QY 181 ctgtccccaatagttctctccagcgaggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 240
Db 260 ctgtccccaatagttctctccagcgaggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 319
QY 241 ggtgtaaagtgttttcaagaccaggaagagagtgcttccaccacaagacgtgtgtgtgt 300
Db 320 ggtgtaaagtgttttcaagaccaggaagagagtgcttccaccacaagacgtgtgtgtgt 379
QY 301 ctgcactcaagggttctcactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 360
Db 380 ctgcactcaagggttctcactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 439
QY 361 acaaggtcaagaactgtgacaaaagaaggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 420
Db 440 acaaggtcaagaactgtgacaaaagaaggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 499
QY 421 tcagaagaagtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 480
Db 500 tcagaagaagtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 559
QY 481 tgtgaatgtgaagaagagagagagagtgctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 540
Db 560 tgtgaatgtgaagaagagagagagagtgctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 619
QY 541 ggagacatctctgtgaccccgccctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 600
Db 620 ggagacatctctgtgaccccgccctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 679
QY 601 catctctctctctctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 660
Db 680 catctctctctctctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 739
QY 661 gtcctgtctctctgtgttaaacgggagagaaactcgtatataatcaaac 720
Db 740 gtcctgtctctctgtgttaaacgggagagaaactcgtatataatcaaac 799
QY 721 attatgagaccagtaacaaactactcaagagagagatgctgtacgacgattccaga 780
Db 800 attatgagaccagtaacaaactactcaagagagagatgctgtacgacgattccaga 859
QY 781 agaaagaagaagagatgtgactgtgaactgtgaactgaaggcgtgttgagactt 838
Db 860 agaaagaagaagagatgtgactgtgaactgtgaactgaaggcgtgttgagactt 917

RESULT 5
209769
ID Z09769 standard; cDNA; 1439 BP.
XX
AC Z09769;

```

XX 18-NOV-1999 (first entry)
XX
XX
DE Human CD137 cDNA.
XX
XX CD137; monocyte growth factor; proliferation; peripheral monocyte;
XX treatment; disease; antitumor; antibacterial; antiviral; antifungal;
XX immunostimulatory; non-specific immune response; phagocytosis;
XX intracellular destruction; microorganism; immune complex; antibody;
XX cytotoxicity; tumor cell; macrophage; hematopoietic system; leucopenia;
XX chemotherapy; radiation; therapy; wound healing disorder; tumor; fungal;
XX bacterial; viral infection; immunosuppressant; gene therapy; human; ds.
OS Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT 140..907.
FT /*tag= a
FT /product= "CD137"
XX
XX WO9944629-A2.
XX
XX 10-SEP-1999.
XX
XX 05-MAR-1999; 99WO-EP01440.
XX
XX 05-MAR-1998; 98EP-0103859.
XX
XX (MERC) MERCKLE GMBH.
XX
XX Schwarz H, Langstein J;
XX WPI: 1999-550983/46.
XX P-PSDB: Y33214.
XX
XX Use of monocyte growth factor CD137 for stimulating proliferation of
XX peripheral monocytes, particularly for treating immune deficiency, e.g.
XX following cancer therapy -
XX
XX Disclosure: Flg 1A; 57pp; German.
XX
XX This invention describes a novel use of the human monocyte growth factor
XX CD137, or its functional analogs, for (i) stimulating proliferation of
XX peripheral monocytes; and (ii) treating diseases that are associated with
XX disorders of a cellular system that includes monocytes (and/or their
XX derived cells, precursor or progenitors) or where the origin and/or
XX progression is treatable by stimulating proliferation of such cells. The
XX products of the invention have antitumor, antibacterial, antiviral,
XX antifungal and immunostimulatory activity. Stimulating proliferation of
XX monocytes promotes the non-specific immune response, i.e. It increases
XX phagocytosis and intracellular destruction of microorganisms. Immune
XX complexes and damaged cells, and improves antibody (in)dependent
XX cytotoxicity to tumor cells. CD137 is used, in vivo or ex vivo, to treat
XX diseases associated with a defective immune response where caused by
XX inadequate numbers of active monocytes/macrophages, especially damage to
XX the hematopoietic system (leucopenia) caused by chemotherapy or radiation
XX therapy; disorders of wound healing (e.g. in dialysis or diabetic
XX patients, or those with chronic venous insufficiency); tumors; bacterial,
XX fungal or viral infections; (non-)congenital or (non-)inherited diseases
XX or injury to the immune system; injury induced by treatment with
XX immunosuppressants (e.g. patients with chronic arthritis or autoimmune
XX disease, or transplant patients). Nucleic acid encoding (I) can be used
XX similarly, in gene therapy procedures. Proliferation of peripheral
XX monocytes is achieved independently of hematopoietic stem cells. This
XX sequence encodes the human CD137 protein described in the method of
XX the invention.
XX
XX Sequence 1439 BP: 394 A: 340 C: 341 G: 364 T: 0 other:

Query Match 99.8%; Score 836.4; DB 20; Length 1439;
Best Local Similarity 99.9%; Pred. No. 1,2e-261;
Matches 837; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 aatcagcttctgctagatcatactctgtccagatttcatactggaagaacgctgttaca 60
DB 100 aatcagcttctgctagatcatactctgtccagatttcatactggaagaacgctgttaca 159
QY 61 catagtagcaccctctgtctgttcccaacttggaggaacaagttcatctgaagattcc 120
DB 160 catagtagcaccctctgtctgttcccaacttggaggaacaagttcatctgaagattcc 219
QY 121 ttgttaactgtcccgccgtgtacattctgtgaataaagaatcaagatttgcagttcc 180
DB 220 ttgttaactgtcccgccgtgtacattctgtgaataaagaatcaagatttgcagttcc 279
QY 181 ctgtcctccaatagtttctccagcgagtggaacaagaacctgtgacataltgcagca 240
DB 280 ctgtcctccaatagtttctccagcgagtggaacaagaacctgtgacataltgcagca 339
QY 241 gtgttaagggtttttagagaccggaaggagtgttctccaccaggaatggcaggtgta 300
DB 340 gtgttaagggtttttagagaccggaaggagtgttctccaccaggaatggcaggtgta 399
QY 301 ctgcacaccaggggttccactgtcctggggcaagatgcagcatgtgtgaacagattgttaa 360
DB 400 ctgcacaccaggggttccactgtcctggggcaagatgcagcatgtgtgaacagattgttaa 459
QY 361 acaaggccaagaacttgacaacaaaagggttgtaagaactgtgtcttggacatttaacga 420
DB 460 acaaggccaagaacttgacaacaaaagggttgtaagaactgtgtcttggacatttaacga 519
QY 421 tcagaagaactgtgcatctgttcgaacctggacaaacttcttggatggagaagctgtgct 480
DB 520 tcagaagaactgtgcatctgttcgaacctggacaaacttcttggatggagaagctgtgct 579
QY 481 tgtgaatggagcaagaagagagagacgtgtctgttgacacatccacagctgcactctcc 540
DB 580 tgtgaatggagcaagaagagagagacgtgtctgttgacacatccacagctgcactctcc 639
QY 541 gggagacatcctctgtgaccccgctgccttcgagagagccaggaactctccagat 600
DB 640 gggagacatcctctgtgaccccgctgccttcgagagagccaggaactctccagat 699
QY 601 catctccttcttctgtgcgtgacgtgcagctgtgtcttcttcttcttcttctac 660
DB 700 catctccttcttctgtgcgtgacgtgcagctgtgtcttcttcttcttcttctac 759
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DB 760 gctcgttctctgtgtttaaacggggcagaagaactcctgtatataatcaacaacc 819
QY 721 attatgagaccagttacaactactcaagaagagaatggctgtagctgcagattccaga 780
DB 820 attatgagaccagttacaactactcaagaagagaatggctgtagctgcagattccaga 879
QY 781 agaagaagaagaagatgtgtaactgtgaatggaatgaatgggtgttggaactt 838
DB 880 agaagaagaagaagatgtgtaactgtgaatggaatgaatgggtgttggaactt 937

RESULT 6
208961
ID 208961 standard; cDNA: 838 BP.

XX 208961;

XX 13-OCT-1999 (first entry)

XX Human receptor protein 4-1BB cDNA.

XX Human receptor protein 4-1BB; H4-1BB; T cell activation; proliferation;
XX mouse 4-1BB cDNA; monoclonal antibody; immune response;
XX organ transplantation; autoimmune disease; diabetes; cancerous tumour;
XX rheumatoid arthritis; lupus; nerve growth factor receptor; ds.

OS	Homo sapiens.
XH	
FH	Key Location/Qualifiers
FT	CDS 41..808
FM	/tag= a
XX	/product= "H1-4AB receptor"
PX	MW9936093-A1.
XX	
PD	22-JUL-1999.
PF	14-JAN-1999; 99WO-US00823.
PR	14-JAN-1998; 98US-0007097.
PA	(ADRE-) ADVANCED RES & TECHNOLOGY INST. (KWON/) KWON B S.
PI	Kwon BS;
XX	
DR	WPJ: 1999-444325/37.
PP	P-PDB: Y28688.
PT	Using human receptor protein 4-1BB ligands to, e.g., treat Diabetes Mellitus, Rheumatoid Arthritis and Systemic Lupus Erythematosus
PS	Disclosure; Pages 76-77; 86pp; English.
CC	The present sequence encodes human receptor protein 4-1BB. 4-1BB is structurally related to members of the nerve growth factor receptor. It contains a putative zinc finger structure similar to that of yeast cIrf-2B protein. Probes derived from mouse 4-1BB cDNA are used to isolate cDNA of H4-1BB. The H4-1BB protein, its ligands, and various monoclonal antibodies have therapeutic uses. They may be used to enhance or suppress T cell activation and proliferation; B cell proliferation; treating cancerous tumours and AIDS. The use of H4-1BB to block H4-1BB ligand binding has practical application in the suppression of immune system during organ transplantation or against autoimmune diseases including diabetes, rheumatoid arthritis, and lupus.
SQ	Sequence 838 BP; 217 A; 192 C; 216 G; 213 T; 0 other;
-	Query Match 99.2%; Score 831.6; DB 20; Length 838; Best Local Similarly 99.5% Pred. No. 3.2e+260; Matches 834; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY	1 aaatagcttgcagtacatacactgtgccaaggatttcacatcggaagaacctgttaaca Db 1 aaatagctttgcatgatcacaccctgcgaagattccatcaatggaaaacagtgtaa 60
OY	61 catagtagccactctgttgtlctcccaacttggagagacaaatcatactcagatccc Db 61 catagtagccactctgttgtlctcccaacttggagagacaaatcatactcagatccc 120
OY	121 ttgtagtaactgccagctggttacattctgtgataaatcaagaatcagatttgcagttc Db 121 ttgtagtaactgccagctggttacattctgtgataaatcaagaatcagatttgcagttc 180
OY	181 ctgtcccccaaatagttttcccaagcgaggtgaaacaaaaggactctgtgatatgcaagca Db 181 ctgtcccccaaatagttttcccaagcgaggtgaaacaaaaggactctgtgatatgcaagca 240
OY	241 gtgtcaaaagtgatttccagaccaagaagagtgcttccccaacagaatgcaagatgtga Db 241 gtgtcaaaagtgatttccagaccaagaagagtgcttccccaacagaatgcaagatgtga 300
OY	301 ctgcactccaaaggtttctaactgcttgagggaagatgcaagcatgtgtgaacagatgtlaa Db 301 ctgcactccaaaggtttctaactgcttgagggaagatgcaagcatgtgtgaacagatgtlag 360
OY	361 acaaaggtcagaagaatgcaaaaaaagtgtaaaagctgttgtcttggagattaaga 420

D	b		361	acaagctcaagaactcgacaaaaaaagtgttgaagaactgttgctttgggacatttaaca	420			
O	y		421	tcaagaacgtgycatcgtctgcacccttgacaaaactgtctcttggalbgaaagtcgtgc	480			
D	b		421	tcaagaacgtgycatcgtctgcacccttgacaaaactgtctcttggalbgaaagtcgtgc	480			
O	y		481	tgtgaatggagcagaaggagagagcgctggtctgtgacacatccacgtcacctctccc	540			
D	b		481	tgtgaatggagcagaaggagagagcgctggtctgtgacacatccacgtcacctctccc	540			
O	y		541	gggaacatccccctgtgacccccctgccccctgcagagagacagaacctccgcagat	600			
D	b		541	gggaacatccccctgtgacccccctgccccctgcagagagacagaacctccgcagat	600			
O	y		601	caticctctcttcttgccgtcgaactgcagtcgcttccctccctgctgtcttccctac	660			
D	b		601	caticctctcttcttgccgtcgaactgcagtcgcttccctccctgctgtcttccctac	660			
O	y		661	gtccgcttctctctgttgttaaacygggcagaagaacctcgtatatataccaacacc	720			
D	b		661	gtccgcttctctctgttgttaaacygggcagaagaacctcgtatatataccaacacc	720			
O	y		721	attatggaccagtatacaactactcaagaaggagatgctgttagctgcgcgatllccaga	780			
D	b		721	attatggaccagtatacaactactcaagaaggagatgctgttagctgcgcgatllccaga	780			
O	y		781	agaagaagaagagagatgtgactgtgaatlgaatlgaaatcaatagagctgtltggacttl	838			
D	b		781	agaagaagaagagagatgtgactgtgaatlgaatlgaaatcaatagagctgtltggacttl	838			
RESULT 7								
ID	Q92086 standard; DNA; 1439 BP.							
XX AC	Q92086;							
XX DT	21-JAN-1996 (first entry)							
DE XX	Human receptor induced by lymphocyte activation (ILA) DNA.							
KW XX	ILA: receptor inducible by lymphocyte activation; disease diagnosis;							
KM XX	antiinflammatory; ss.							
OS XX	Homo sapiens.							
FH FT	Key CDS	Location/Qualifiers						
FT		140..904						
PA		/*tag= a						
PN	CA2108401-A.							
PD	28-MAR-1995.							
PF	14-OCT-1993; 93CA-2108401.							
PR XX	27-SEP-1993; 93US-0127693.							
XX PA	(REGC) UNIV CALIFORNIA.							
XX PL	Lotz M, Schwarz H;							
XX DR	WPI; 1995-194420/26.							
XX DR	P-PSDB; R74087.							
PT PR	New receptor inducible by lymphocyte activation - used to develop							
XX PS	prods. for the diagnosis and treatment of inflammatory host defence							
XX CC	pathology.							
XX	Claim 52; Page 61; 91pp; English.							
CC	This DNA may be expressed recombinantly for the production of ILA.							
CC	The cDNA was isolated from a library constructed from activated							

CC human T-lymphocyte leukemia virus type-1 transformed human T-
 CC lymphocytes.
 XX
 SQ Sequence 1439 BP; 393 A; 336 C; 346 G; 364 T; 0 other;

Query Match 98.9%; Score 828.4; DB 16; Length 1439;
 Best Local Similarity 99.3%; Pred. No. 4,8e-259;
 Matches 832; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 aatcagcttgtagatatacctgtgcagattcatcatatggaagacgtgttaca 60
 |||||||
 DB 100 aatcagcttgtagatatacctgtgcagattcatcatatggaagacgtgttaca 159
 QY 61 catagtagcactctgtctgtctcctcaactttgagagacaagatcatcagagatcc 120
 |||||||
 DB 160 catagtagcactctgtctgtctcctcaactttgagagacaagatcatcagagatcc 219
 QY 121 ttgttagtaactgccagcgtgtaacttctgtataataacaggaatcagatttcagttcc 180
 |||||||
 DB 220 ttgttagtaactgccagcgtgtaacttctgtataataacaggaatcagatttcagttcc 279
 QY 181 ctgtctcccaataagtttctcagcaggtgagacaagacgtgtgacataatgcagca 240
 |||||||
 DB 280 ctgtctcccaataagtttctcagcaggtgagacaagacgtgtgacataatgcagca 339
 QY 241 ggttaaggtgttttcaagagcagaagagtgcttctcaccagcaatgcagatgtga 300
 |||||||
 DB 340 ggttaaggtgttttcaagagcagaagagtgcttctcaccagcaatgcagatgtga 399
 QY 301 ctgcaactcagaggttctcaactgtggtgagagatgacatgtgtgacagagatgtga 360
 |||||||
 DB 400 ctgcaactcagaggttctcaactgtggtgagagatgacatgtgtgacagagatgtga 459
 QY 361 acaaggtcagaactgcagcaaaaaaggtgttaagacttctccttgagacatttaaga 420
 |||||||
 DB 460 acaaggtcagaactgcagcaaaaaaggtgttaagacttctccttgagacatttaaga 519
 QY 421 tcaagaacgtgcatctgtcgaacctgtgacaactgttcttggatgtaaaatctgtgt 480
 |||||||
 DB 520 tcaagaacgtgcatctgtcgaacctgtgacaactgttcttggatgtaaaatctgtgt 579
 QY 481 tttgtaattggaagaggaaggaagtgctgtgtgacacattccagctgacctctcc 540
 |||||||
 DB 580 tttgtaattggaagaggaaggaagtgctgtgtgacacattccagctgacctctcc 639
 QY 541 gggagacatcctctgtgaccccgctgccttcgagaagagcagagacattccgagat 600
 |||||||
 DB 640 gggagacatcctctgtgaccccgctgccttcgagaagagcagagacattccgagat 699
 QY 601 catctcctcttcttctgctgacgtgcagctgtgtccttctcctgcttctcctcac 660
 |||||||
 DB 700 catctcctcttcttctgctgacgtgcagctgtgtccttctcctgcttctcctcac 759
 QY 661 gctcgttcttctgtgtttaaagcgaggaagaacacctgtatataatcaaacacc 720
 |||||||
 DB 760 gctcgttcttctgtgtttaaagcgaggaagaacacctgtatataatcaaacacc 819
 QY 721 attatgacacagatatacactaccacaagagaatgctgtagctgcagatttcaga 780
 |||||||
 DB 820 attatgacacagatatacactaccacaagagaatgctgtagctgcagatttcaga 879
 QY 781 aagaagaagaagagatgtgaactgtgaatggaatcacaatagggctgttggacttt 838
 |||||||
 DB 880 aagaagaagaagagatgtgaactgtgaatggaatcacaatagggctgttggacttt 937

RESUME 8
 ID T88969
 XX T88969 standard; DNA: 946 BP.
 AC T88969;
 XX

DT 01-APR-1998 (first entry)
 XX
 DE DNA encoding a human h4-1BSV receptor.
 XX
 KW h4-1BSV receptor; 4-1BB receptor splicing variant; endotoxic shock;
 KW tumour necrosis factor; TNF ligand; T-cell activation; inflammation;
 KW tumour prevention; viral infection; autoimmune disease;
 KW cellular proliferation; ss.
 XX
 OS Homo sapiens.

FT	Key	Location/Qualifiers
FT	CDS	124..783
FT	sig_peptide	/tag= a
FT		124..177
FT		/tag= b
FT		/note= "putative"
FT	mat_peptide	178..780
FT		/tag= c

WO9733898-A1.
 18-SEP-1997.
 PD
 XX
 PF 15-MAR-1996; 96WO-US03587.
 PR
 XX
 PA 15-MAR-1996; 96WO-US03587.
 (HUMA-) HUMAN GENOME SCI INC.

Gentz RL, Ni J, Yu G;
 PI
 XX
 DR WPI; 1997-470806/43.
 DR P-PSDB; W31759.

PT Human 4-1BB receptor splicing variant and related DNA - used to
 PT develop products for treating e.g. tumours, viral infection,
 PT endotoxic shock, autoimmune disease or bone resorption.
 PS
 XX
 Claim 8; Fig 1; 73pp; English.

CC The present sequence encodes a novel human h4-1BSV receptor. This is a
 CC human 4-1BB receptor splicing variant. The 4-1BB ligand is a member of
 CC the tumour necrosis factor (TNF) family of ligands. It is induced by
 CC T-cell activation. The h4-1BSV receptor nucleic acid and protein can be
 CC used for diagnosis and therapy. In particular, agonists of h4-1BSV
 CC receptor can be used to treat and/or prevent tumours, restenosis,
 CC cytotoxicity, bacterial and viral infection, deleterious effects of
 CC ionising radiation, autoimmune disease, AIDS and graft-host rejection,
 CC to regulate immune responses, wound healing and cellular proliferation.
 CC Antagonists can be used to treat and/or prevent endotoxic shock,
 CC inflammation, cerebral malaria, activation of the HIV virus, graft
 CC rejection, bone resorption and cachexia.
 XX
 SQ Sequence 946 BP; 257 A; 218 C; 230 G; 241 T; 0 other;

Query Match 72.6%; Score 608.8; DB 18; Length 946;
 Best Local Similarity 86.9%; Pred. No. 9.1e-188;
 Matches 728; Conservative 0; Mismatches 2; Indels 106; Gaps 1;

QY 1 aatcagcttgtagatatacctgtgcagattcatcatatggaagacgtgttaca 60
 |||||||
 DB 84 aatcagcttgtagatatacctgtgcagattcatcatatggaagacgtgttaca 143
 QY 61 catagtagcactctgtctgtctcctcaactttgagagacaagatcatcagagatcc 120
 |||||||
 DB 144 catagtagcactctgtctgtctcctcaactttgagagacaagatcatcagagatcc 203
 QY 121 ttgttagtaactgccagcgtgtaacttctgtataataacaggaatcagatttcagttcc 180
 |||||||
 DB 204 ttgttagtaactgccagcgtgtaacttctgtataataacaggaatcagatttcagttcc 222

```
QY 181 ctgtccccaatagtttctccagcgaggtgacaagaacctgtgacatatcgagca 240
Db 223 -----
QY 241 gtgtaaagtggttttcaggaccaaggaagtggtctctccaccagcaatgagatgtga 300
Db 223 -----gtgttttcaggaccaaggaagtggtctctccaccagcaatgagatgtga 275
QY 301 ctgcactccagggtttcactgctctgaggcgagatgacagatgtgtgaacagatgttaa 360
Db 276 ctgcactccagggtttcactgctctgaggcgagatgacagatgtgtgaacagatgttaa 335
QY 361 acaaggtcaagaactgacacaaaagggttgaagaactgtgtgtgttgagacattaa 420
Db 336 acaaggtcaagaactgacacaaaagggttgaagaactgtgtgtgttgagacattaa 395
QY 421 tcgaaaaagtggtgcatctgtgaccccttgacaactgtttcttgatgtgaagatgtgct 480
Db 396 tcgaaaaagtggtgcatctgtgaccccttgacaactgtttcttgatgtgaagatgtgct 455
QY 481 tgtgaatggagacgaaggagagagcgtgtctgtgacacatctcagctgacctctcc 540
Db 456 tgtgaatggagacgaaggagagagcgtgtctgtgacacatctcagctgacctctcc 515
QY 541 gggagcatcctctgtgaccccgctgcccctgagagagcaggaacatctccgagat 600
Db 516 gggagcatcctctgtgaccccgctgcccctgagagagcaggaacatctccgagat 575
QY 601 catctcctcttcttctgctgagctgagctgagctgtgtctctctgctgcttctccac 660
Db 576 catctcctcttcttctgctgagctgagctgagctgtgtctctctgctgcttctccac 635
QY 661 gctcgttctctgtgtttaaaccgggcaagaagaacatctctgatatataatcaacaacc 720
Db 636 gctcgttctctgtgtttaaaccgggcaagaagaacatctctgatatataatcaacaacc 695
QY 721 attatgagaccagtaacaactactcaagaggaagatggtctgtagctgtgcgattcca 780
Db 696 attatgagaccagtaacaactactcaagaggaagatggtctgtagctgtgcgattcca 755
QY 781 agaaagaagaagaagatgtgtaactgtgaatggaatgaatgaatgaatgaatgaatga 838
Db 756 agaaagaagaagaagatgtgtaactgtgaatggaatgaatgaatgaatgaatgaatga 813

RESULT 9
X02162
ID X02162 standard; DNA; 946 BP.
XX
AC X02162;
XX
DT 23-APR-1999 (first entry)
XX
DE Human h4-1BBSV receptor DNA.
XX
KW h4-1BBSV receptor; human; splice variant; antagonist; treatment;
KW disease prevention; endotoxic shock; inflammation; cerebral malaria;
KW HIV virus activation; graft rejection; bone resorption; cachexia;
KW gene therapy; ss.
XX
OS Homo sapiens.
XX
FH Key 124..783 Location/Qualifiers
FT CDS 124..783
FT /tag= a
FT /product= "h4-1BBSV"
FT sig_peptide 124..177
FT /tag= b
FT mat_peptide 178..780
FT /tag= c
XX
PN US5874240-A.
XX
```

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PD 23-FEB-1999.
XX
PF 13-MAR-1997; 9705-0816605.
XX
PR 15-MAR-1996; 9605-0013474.
PR 13-MAR-1997; 9705-0816605.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Dillon PJ, Gentz R, Ni J, Yu G;
XX
DR WPI: 1999-179974/15.
DR P-PSDB; W92523.
XX
PT New nucleic acid encoding human 4-1BB receptor splicing variant -
PT useful in treating h4-1BBSV mediated disease states such as
PT endotoxic shock, inflammation, graft rejection and inactivation of
PT HIV
XX
PS Claim 11; Fig 1A-B; 28pp; English.
XX
CC This sequence encodes a novel human h4-1BBSV receptor protein which is
CC used in a method for making a human 4-1BB receptor splice variant which
CC acts as an antagonist. The antagonist polypeptides may be used to
CC treat/prevent disease states mediated by h4-1BBSV receptors such as
CC endotoxic shock, inflammation, cerebral malaria, activation of the HIV
CC virus, graft rejection, bone resorption and cachexia. The h4-1BBSV
CC coding sequences are useful in gene therapy.
XX
SQ Sequence 946 BP; 257 A; 218 C; 230 G; 241 T; 0 other:

Query Match 72.6%; Score 608.8; DB 20; Length 946;
Best Local Similarity 86.9%; Pred. No. 9.1e-188;
Matches 728; Conservative 0; Mismatches 2; Indels 108; Gaps 1;

QY 1 aatagcttgctagatcatcaactgtgacagatttcaatcattggaagaacagctgttaca 60
Db 84 aatagcttgctagatcatcaactgtgacagatttcaatcattggaagaacagctgttaca 143
QY 61 catgtatgcaactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 120
Db 144 catgtatgcaactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 203
QY 121 ttgtatgtaactgcccagctgtacattctgtgataatacagaatcagatttcagttcc 180
Db 204 ttgtatgtaactgcccagctgtacattctgtgataatacagaatcagatttcagttcc 222
QY 181 ctgtccccaatagtttctccagcgaggtgacaagaacctgtgacatatcgagca 240
Db 223 -----
QY 241 gtgtaaagtggttttcaggaccaaggaagtggtctctccaccagcaatgagatgtga 300
Db 223 -----gtgttttcaggaccaaggaagtggtctctccaccagcaatgagatgtga 275
QY 301 ctgcactccagggtttcactgctctgaggcgagatgacagatgtgtgaacagatgttaa 360
Db 276 ctgcactccagggtttcactgctctgaggcgagatgacagatgtgtgaacagatgttaa 335
QY 361 acaaggtcaagaactgacacaaaagggttgaagaactgtgtgtgttgagacattaa 420
Db 336 acaaggtcaagaactgacacaaaagggttgaagaactgtgtgtgttgagacattaa 395
QY 421 tcgaaaaagtggtgcatctgtgaccccttgacaactgtttcttgatgtgaagatgtgct 480
Db 396 tcgaaaaagtggtgcatctgtgaccccttgacaactgtttcttgatgtgaagatgtgct 455
QY 481 tgtgaatggagacgaaggagagagcgtgtctgtgacacatctcagctgacctctcc 540
Db 456 tgtgaatggagacgaaggagagagcgtgtctgtgacacatctcagctgacctctcc 515
QY 541 gggagcatcctctgtgaccccgctgcccctgagagagcaggaacatctccgagat 600
```

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Db 516 gggagacatcctctgtacccgcctgcctctgagagagcaggacatctccgcagat 575
      |||
Qy 601 catctcctctctctctgcgtacgtcgtactgctgtctctctctctctctctac 660
      |||
Db 576 catctcctctctctctgcgtacgtcgtactgctgtctctctctctctctctac 635
      |||
Qy 661 gctccgtctctctgtgttaaacgggacgaagaactctgtatatattcaaacacc 720
      |||
Db 636 gctccgtctctctgtgttaaacgggacgaagaactctgtatatattcaaacacc 695
      |||
Qy 721 attatagagaccagtaacactactcaagagagatgctgtactgctccgattccaga 780
      |||
Db 696 attatagagaccagtaacactactcaagagagatgctgtactgctccgattccaga 755
      |||
Qy 781 agaagaagaagaagatgtgtactgtgaaatggaagtcaataagagctgttggagctt 838
      |||
Db 756 agaagaagaagaagatgtgtactgtgaaatggaagtcaataagagctgttggagctt 813

RESULT 10
T39541
ID T39541 standard; cDNA to mRNA; 2347 BP.
XX
AC T39541;
XX
DT 12-DEC-1996 (first entry)
XX
DE Mouse receptor 4-1BB cDNA.
XX
KW Receptor 4-1BB; HA-1BB; monoclonal antibody; T-lymphocyte; T-cell;
KW Immunostimulant; Cancer; autoimmune disease; graft rejection;
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT CDS 146..916
FT mat_peptide /tag= a
FT 146..913
FT /tag= b
XX
PN W09629348-A1.
XX
PD 26-SEP-1996.
XX
PF 22-MAR-1996; 96WO-US033965.
XX
PR 23-MAR-1995; 95US-0409851.
XX
PA (INDV ) UNITV INDIANA FOUND.
XX
PI Kang C, Kwon BS;
XX
DR MPI; 1996-443138/44.
DR P-PSDB; W04173.
XX
PT Monoclonal antibody specific for human receptor protein 4-1BB - used
PT to enhance proliferation and activation of T-cells for treatment of
PT cancer and to inhibit specific ligand binding for treating
PT auto-immune diseases
XX
PS Disclosure; Page 32-34; 48pp; English.
XX
CC A cDNA clone (T39541) codes for novel murine receptor protein
CC 4-1BB (W04173), a protein that has the potential to function as
CC an accessory signaling molecule during T-cell activation and
CC proliferation. The cDNA clone was isolated and identified by
CC specific expression of T-cell genes. Primers (see also T39542-45)
CC based on the murine 4-1BB cDNA were utilised in the identification
CC of the gene (see also T39546) for the human homologue HA-1BB
CC (W04174), a protein used to raise a monoclonal antibody useful
CC in cancer and autoimmune disease therapy.

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XX
SQ Sequence 2347 BP; 590 A; 570 C; 580 G; 607 T; 0 other;

Query Match          40.5%; Score 339.2; DB 17; Length 2347;
Best Local Similarity 67.8%; Pred. No. 6,7e-100;
Matches 537; Conservative 0; Mismatches 243; Indels 12; Gaps 4;

Qy 14 agtatacactctgtgcagatttcaatcgtggaacacgtgttacaacatagtgccact 73
      |||
Db 119 agtctcgtgcagatgtgacatttcgcattcgtggaacacgtgttacaacatagtgctact 178
      |||
Qy 74 ctgtgtgtgttcccaactttgaaaggaacaagatcatctgcagtgacttctgtgaatctc 133
      |||
Db 179 gtctgtgtctagtgagctcttgaaaggttggaagccctgcgaactctctgtataactgt 238
      |||
Qy 134 ccaagctgtatcatctctgtataaagaagatcagaatttcgaatccctgcctcccaat 193
      |||
Db 239 cagcctgtactctctgcagaaaatac---aatcagctgcgaagagctgcctcccaagt 295
      |||
Qy 194 agttctccagcgcaggtgagacaagaagaccctgtacatatgcagcaggtglaaagtgct 253
      |||
Db 296 acccttccagcataggttgacacagccgaactgtacaatctgcagaggtgtgcaggtcat 355
      |||
Qy 254 ttcagaacccaagaagagtgcttccctccacaagaatgcagagtgtagctcaactccagg 313
      |||
Db 356 ttcaggttcaagaagatttctcctctaccacaacgcgagtgtagtgattgaaaga 415
      |||
Qy 314 ttcacagctctggggagagatgcagatgtgtgaaagatgtglaaagtglaaagtgcaaga 373
      |||
Db 416 ttcattgtcttgaggccacagtgcaacagatgtgaaagactgtgacgttgcgtgcgaag 475
      |||
Qy 374 ctgacaaaagaagctgtglaaagactgtgtcttctggaacattcaacgtatcaagaacg---t 430
      |||
Db 476 ctacaggaagcaggttgtaacaaactgtagcttgggaacatttaatgcaggaacgttact 535
      |||
Qy 431 ggcactgtctgcagccctgcagacaactgtcttctggaatggaagtgctgtgtaatggg 490
      |||
Db 536 ggcgtctgtgcagccctgcagacaactgtctcttagagcgaagtgctgtcttaagaacggg 595
      |||
Qy 491 acgaagaagaagagcgtgtgtgtggaacatctcccaactgacactctccgggagcatcc 550
      |||
Db 596 accaaggaagaagacgtgtgtgtggaacccctgtgtgtgagcttctcccaag---taac 652
      |||
Qy 551 tctgtgaccccgctgcctctgcagagagccaggaactctcccgagatcatctcttc 610
      |||
Db 653 accatttctgtgactccagaggggagccagaggaactctccctgcaggttccctacttg 712
      |||
Qy 611 ttctctgcctgcagctgcagctgtgtctctctctgtcttctctcctcaagctcgtttc 670
      |||
Db 713 ttctctgcctgcagctgcagctgtgtctctctgtcttctctcctcaactctctctctc 769
      |||
Qy 671 tctgtgttaaacggggcagaagaactctctgtatatattcaaacacattataga 730
      |||
Db 770 tctgtgtcctaattggaatcagaagaataatctcccaactatccaagcaacatttaagaag 829
      |||
Qy 731 ccagtaacaactactcaagaaggaagatgtgtgagctgcgcgattccagaagaagaagaa 790
      |||
Db 830 accaactggagcagctcaagaaggaagatgtgtgagctgcgcgattccagaagaagaagaa 889
      |||
Qy 791 ggaagatgtgaa 802
      |||
Db 890 ggaaggaagaga 901
      |||

RESULT 11
086127
ID 086127 standard; cDNA; 2350 BP.
XX
AC 086127;
XX
DT 16-OCT-1995 (first entry)
XX

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DE 4-1BB receptor protein cDNA.
XX
XX 4-1BB; receptor protein; immunosuppressive; autoimmune disease;
KM organ transplantation; cell membrane ligand; ss.
XX
OS Mus sp.
XX
XX Key Location/Qualifiers
FH CDS 146..916
FT sig_peptide 146..214
FT mat_peptide 215..913
FT
FT /tag= c
FT /product= 4-1BB receptor protein
FT misc_difference 1253..1255
FT /tag= d
FT /note= "bases n at positions 1253-1255 are not
FT identified in the specification"
FT polyA_signal 1303..1308
FT /tag= e
XX
XX W09507984-A.
XX
XX PD 23-MAR-1995.
XX
XX PF 15-SEP-1994; 94WO-US10457.
XX
XX PR 16-SEP-1993; 93US-0122796.
XX
XX (INDV ) UNIV INDIANA FOUND.
XX
XX PA
XX PI
XX P1
XX Kwon BS;
XX
XX DR WPI: 1995-131352/17.
XX P-PSDB; R70978.
XX
XX DR
XX
XX PT Novel cDNA encoding human receptor protein H4-1BB - useful to
PT produce the protein which is used to treat auto-immune disease
PT and facilitate organ transplantation
XX
XX PS Disclosure; Fig.1; 36pp; English.
XX
XX CC PCR primers based on the mouse receptor protein 4-1BB gene, given in
CC 086127, were used to probe a cDNA library of activated human T-cells
CC to isolate the homologous human gene. H4-1BB (086126).
XX
XX Sequence 2350 BP; 590 A; 559 C; 591 G; 607 T; 3 other:
SQ

```

Query Match 40.3%; Score 337.6; DB 16; Length 2350;
Best Local Similarity 67.7%; Pred. No. 2.2e-99;
Matches 536; Conservative 0; Mismatches 244; Indels 12; Gaps 4;

```

QY 14 agtatacatcctgtgcccagatttcatactggaacagctgttacaacatagtagccact 73
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 119 agtgcctgtgcatgtgacatcgcgcattggaacaaactgttaacagtggtgtcatt 178
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 74 ctgtgtgtgtgtcccaactttgagagagaacatcattgcagagatcctgtagtaactgc 133
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 179 gtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 238
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 134 ccagctgtgtacatctgtgataataacagagatcagatttcagctcctgtccccaat 193
   | ||||| ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| |||||
DB 239 cagctgtgtactctctcgaagaataac--aatcagctgtcgaagagctgcctccaagt 295
   | ||||| ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| |||||
QY 194 agttctccagcgcaggtggaacaagacctgtgacatatacagagcaagtgttaaagtgt 253
   | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 296 accctctccagcatagtgagcagccgcagactgtaacatctgcagagtgtgtgcaggtcat 355
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 254 ttccagacagaagagagtgcttctccacacagcaatgcagagtgtgactgcaactccagg 313
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 356 ttccagttcaagaagtttgtctctctaccaccaacagcgcaggtgtgagtgatcattgaaga 415

```

```

QY 314 ttccactgccttggggccagagatgcagcatgtgtgtaacaaggattgttaacaagttcaagaa 373
   ||| ||| ||||| ||| ||||| ||| ||||| ||||| ||||| ||||| ||||| |||||
DB 416 ttccattctcgttggggccacagatgtcacccagatgtgtaaaagatcagagcctcggccaagag 475
   ||| ||| ||||| ||| ||||| ||| ||||| ||||| ||||| ||||| ||||| |||||
QY 374 ctgacaaaaaaaggtgttaaaagactgtgtcttcttgagacatttaacgatacagaacag--t 430
   ||| ||| ||||| ||| ||||| ||| ||||| ||||| ||||| ||||| ||||| |||||
DB 476 ctacgaaagcaggtgttgcaaaaacctgtagcttgggaacatttaacgatacagaacgtagct 535
   ||| ||| ||||| ||| ||||| ||| ||||| ||||| ||||| ||||| ||||| |||||
QY 431 ggcattctgcagcccttggaacaacatcgttctcttgatgtgaaagtcgtgtctgtgtgaatgg 490
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 536 ggggtctgtgcagcccttgagcgaacatgcctcttgaacggaagtgctgtgtttaagaacggg 595
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 491 acgaaggaagagagcgtgtgtgtgtgagacatctccagctgcagctctctccgggagacatcc 550
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 556 accaaggagaagagagcgtgtgtgtgtgagccctctgtgtgtgagcttctctccag---tacc 652
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 551 tctgtgaccccgccctgtccctctcgagagagccagacacatctccgacagatcatctccttc 610
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 653 accattctgtgactccagagggagaccagagagggacactcctctgagttccttactctg 712
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 611 ttcttgcgtgacgttgacgtgtgtgtctctcctgctgttcttcttaagcttcgttc 670
   ||| ||| ||||| ||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||
DB 713 ttccgtggtcgtgacatcg--gcttgcgtgtgcccgtgattcttactctcgtgttc 769
   ||| ||| ||||| ||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||
QY 671 tctgtgttaaacggggaagaagaactcctgtatataatcaaacacacattatgaga 730
   ||||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 770 tctgtgtcacaattgatacagaaaaaattccccacatatccaagcaacatttaagaag 829
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 731 ccagtaacaactactcaagagagaagatgtgtgtgtagtgcggattccagaagaagaagaa 790
   ||| ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 830 accactgtgagcagctcaagaagaagatgtgtgtagctgtccggtgtccacaagaagaagaa 889
   ||||| ||||| ||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||
QY 791 ggaagatgtgaa 802
   ||||| ||||| ||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||
DB 890 ggaagagaagaga 901
   ||||| ||||| ||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||

```

RESULT 12
X90763
ID X90763 standard; cDNA; 2350 BP.
XX
XX AC X90763;
XX
XX DT 13-OCT-1999 (first entry)
XX
XX DE Mouse receptor protein 4-1BB cDNA.
XX
XX KW Mouse receptor protein 4-1BB cDNA; 4-1BB receptor protein;
KW H4-1BB protein; human 4-1BB protein; T cell activation; proliferation;
KW immune response; autoimmune disease; organ transplantation;
KW cancerous tumour; ss.
XX
XX OS Mus musculus.
XX
XX FH Key Location/Qualifiers
XX FT CDS 146..916
XX FT /tag= a
XX FT /product= "Mouse 4-1BB receptor protein"
XX
XX W09936093-A1.
XX
XX PD 22-JUL-1999.
XX
XX PF 14-JAN-1999; 99WO-US00823.
XX
XX PR 14-JAN-1998; 98US-0007097.
XX
XX PA (ADRE-) ADVANCED RES & TECHNOLOGY INST.
XX PA (KWON/) KWON B S.
XX
XX PI Kwon BS;
XX

DR WPI: 1999-44325/37.
DR P-PSDB; Y28687.

PT Using human receptor protein 4-1BB ligands to, e.g. treat Diabetes
PT Mellitus, Rheumatoid Arthritis and Systemic Lupus Erythematosus
XX
XX
PS Disclosure; Page 74-75; 86pp; English.

CC The present sequence encodes mouse 4-1BB receptor protein. This protein
CC has 65% homology with human receptor protein 4-1BB. Probes derived from
CC mouse 4-1BB cDNA are used to isolate cDNA of H4-1BB. The H4-1BB protein,
CC its ligands, and various monoclonal antibodies have therapeutic uses.
CC They may be used to enhance or suppress T cell activation and
CC proliferation; for activation or inhibition of immune response; to block
CC H4-1BB ligand binding; treating cancerous tumours and autoimmune
CC diseases; and during organ transplantation.

XX
SQ Sequence 2350 BP; 590 A; 562 C; 589 G; 606 T; 3 other;

Query Match 40.3%; Score 337.6; DB 20; Length 2350;
Best Local Similarity 67.7%; Pred. No. 2.2e-99;
Matches 536; Conservative 0; Mismatches 244; Indels 12; Gaps 4;

QY 14 agatataactgtgccagattcatcatggaagaacgctgttaacacatagtagccact 73
DB 119 aggtccctgtgcatgtgacattccgcaltggaacaacatgtaacagtggtgcatc 178
QY 74 ctgtgtgtgtccctcaacttgagagacaaatcatcttgagatccctgttaactgc 133
DB 179 gt 238
QY 134 ccagctgtgtacattctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 193
DB 239 cagctgtgtacttctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 295
QY 194 agtttccagcgcaggt 253
DB 296 accttccagcgcaggt 335
QY 254 ttcaagaccaggaagagtttctccacacgaatgcaagtggtgtgtgtgtgtgtgt 313
DB 356 ttcaagttcaagaagattgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 415
QY 314 ttcaatgtcctgt 373
DB 416 ttcaatgtcctgt 475
QY 374 ctgaacaaaagagtggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 430
DB 476 ctgaacgaagcaggt 535
QY 431 ggatctgt 490
DB 536 gggt 595
QY 491 acgaagaggaagagagtggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 550
DB 596 accacgagagagagagtggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 652
QY 551 tctgt 610
DB 653 accatttctgt 712
QY 611 ttctgt 670
DB 713 ttctgt 769
QY 671 tctgt 730
DB 770 tctgt 829
QY 731 ccagttacaactctcaagaggaagatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 790

DB 830 accactggagcagctcaagaaggaagatgtgtgtgtgtgtgtgtgtgtgtgtgtgt 889
QY 791 ggaagatgtgaa 802
DB 890 ggaagaggaagga 901

RESULT 13

Q75428
ID Q75428 standard; cDNA to mRNA; 768 BP.

XX
AC Q75428;

XX
DT 08-AUG-1995 (first entry)

XX
DE Murine 4-1BB polypeptide coding sequence.

XX
KW T-cell; lymphocyte; activation; tissue culture; clone; cell lines;

XX
KM proliferation; stimulation; 4-1BB-L; ligand; receptor; cytokine; ss.

XX
OS Mus musculus.

XX
FH Key Location/Qualifiers

FT CDS 1..768 /tag= a

FT sig_peptide /product= 4-1BB polypeptide.

FT mat_peptide /tag= b

FT /tag= c

PN WO9426290-A.

XX
PD 24-NOV-1994.

XX
PF 06-MAY-1994; 94MO-US05036.

XX
PR 07-MAY-1993; 93US-0060843.

XX
PA (IMV) IMMUNEX CORP.

PI Alderson MR, Goodwin RG, Smith CA;

XX
DR WPI: 1995-022265/03.

XX
DR P-PSDB; R64199.

PT Cytokine, 4-1BB ligand (4-1BB-L) - binds to cell surface receptor

PT 4-1BB to transduce signal

XX
PS Example 1; Page 43-44; 65pp; English.

XX
CC The 4-1BB polypeptide (receptor) and the 4-1BB-L (cytokine, see

CC Q75428) are useful in a pharmaceutical composition for stimulating

CC the immune system. The 4-1BB and 4-1BB-L polypeptides are also useful

CC for exploring mechanisms of T-cell activation, as they are expressed

CC on T lymphocytes. 4-1BB-L can be used as a tissue culture reagent for

CC in vitro cultivation of primary T-cells during the derivation of

CC clonal T-cell lines. It may also be used to stimulate proliferation

CC of activated T-cells, used in therapeutic procedures.

XX
SQ Sequence 768 BP; 188 A; 186 C; 217 G; 177 T; 0 other;

Query Match 39.5%; Score 331.4; DB 16; Length 768;
Best Local Similarity 68.2%; Pred. No. 1.2e-97;
Matches 522; Conservative 0; Mismatches 231; Indels 12; Gaps 4;

QY 41 atgggaacacgctgttacaacatagtagcactctgtgtgtgtgtgtgtgtgtgtgtgtgtgt 100
DB 1 atgggaacacacgtttacaacagtggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 60
QY 101 acaagatcatgtgcagagctctgt 160

Db	61	gtggagcgcgcgcagaaactcctgtgataactgcgtacgacctgtaacttctctgcagaaaaaac	120
QY	161	aggaatcagatttgcagtcctctgtctcctcaaatgatttcttcacgcaggttgcagaaag	220
Db	121	--aatccagctctgaagaagctgtccctcccaagtaactctcttcacagataagttgcagacg	177
QY	221	acctgtgacatagtcagcagttgtaaaagttgttttcaggaccggaaagagtttctctc	280
Db	178	aactgtgaacatctgcaagaagttgtgtgcaggctatttcagtttcagaaagttttctctct	237
QY	281	accagaacatgcagagtgcgtgacgtcacctccagggtttcaactgcctgtggggcagatgcagc	340
Db	238	accaccaacgcggggagttgtgagatgtcattggaagatcattcattgtctgtgggccaagttcac	297
QY	341	atgtgtgcacagagattgttaaaacaagttccaaagaaactgtgacaaanaaagttgttaagactgt	400
Db	298	agatgtgaaaagagactgtgcagcctgtgcgaagagctaaagcagaggtttgcaaacctgtc	357
QY	401	tgctttggaacatttaacgatacgaataacg---tgcatctgttcgacccctgtgacaaactgt	457
Db	358	agcttgcggacaatttaataatgcacgaacacggtactgtgcgtctgtccaccccttgacgaactgc	417
QY	458	tctttggatggaaagctctgtgctgtgtgaatgagacgaagagagacgtgtgtgtgga	517
Db	418	tctctagacggaaagctctgtgtctttaaagaccgcggacacgagagaagacgtgtgtgtgga	477
QY	518	ccatctccagctgcgaactctctccgcggagacacccctctgtgaccccgccctgccctgcgaga	577
Db	478	ccccctgtgtgtgagctctctctcccaag---taccacacattctgtgatacctcaaggagga	534
QY	578	gagccagacacactccgcagatcatctctcttcttctgtgcgtgcagctgcagtcggtg	637
Db	535	ccagagagggccactcccttgtagcttacttactgttctctgtgcgtgcagtcagtcg---gcttgc	591
QY	638	ctcttcctgcgtcttcttctactacgctccggttctctctgtgtttaaaggcgacagaagaaa	697
Db	552	ctgcgtgcctgcgtatcttacttactctctctgttctctctgtgtcctcaatgatacgaagaaa	651
QY	698	ctctgtatataatcaacaacacatttatgagacagtatcaaacactacaagtggaagat	757
Db	652	tccccccacatattccaagaacacatttaagaagaccactgtgagcagctcaagtggaagat	711
QY	758	ggcgtgtagctgcgaattccagaagaagaagaagagatgtgaa	802
Db	712	gtttgtagctgtcgcgattgtccacagaagaagaagaagagagagga	756
RESULT 14			
T91027			
T91027 standard; cDNA to mRNA: 768 BP.			
T91027;			
25-FEB-1998 (first entry)			
Mouse 4-1BB receptor cDNA clone mu4-1BB.			
4-1BB ligand; 4-1BB-L; receptor; mouse; cytokine; T lymphocyte;			
T cell; proliferation; immunostimulant; ss.			
Mus musculus.			
Key			
Location/Qualifiers			
1..69			
/*tag= a			
mat_peptide			
70..768			
/*tag= b			
US5674704-A.			
07-OCT-1997.			

PE	07-MAY-1993;	93US-0060843.
XX		
XX	06-MAY-1994;	94US-0236918.
PR	07-MAY-1993;	93US-0060843.
XX		
PA	(IMMV)	IMMUNEX CORP.
XX		
PI	Alderson MR,	Goodwin RG, Smith CA;
XX		
XX	WPI; 1997-502333/46.	
DR	P-PSDB;	W26659.
XX		
PT	DNA encoding 4-1BB ligand polypeptide(s) - useful for stimulating	
PT	T-cell proliferation in vitro, and as research tools	
XX		
PS	Disclosure; Column 39-40; 32pp; English.	
XX		
CC	This cDNA clone encodes mouse 4-1BB (see W26659), a member of the	
CC	tumour necrosis factor receptor superfamily that is expressed on	
CC	helper, suppressor and cytolytic T lymphocytes, as well as mouse	
CC	brain tissue. A novel claimed cytokine, designated 4-1BB ligand	
CC	(4-1BB-L) has been identified, cloned and sequenced (see W26656)	
CC	that binds to murine 4-1BB. 4-1BB-L, especially its soluble	
CC	extracellular domain, can be used to stimulate T-cell proliferation	
CC	in vitro, as a research tool and as an affinity ligand for	
CC	purifying 4-1BB.	
XX		
SQ	Sequence 768 BP; 188 A; 186 C; 217 T; 0 other;	

Query Match	39.5%	Score 331.4	DB 18	Length 768
Best Local Similarity	68.28	Pred. No. 1.2e-97		
Matches 522; Conservative	0	Mismatches 231;	Indels 12;	Gaps 4

OY	41	atgggaacaacgctgrrtaaacacatagtagcactctgtgtgtgtcctcaactttagag	100
Db	1	atggggaaaaaaactcttaacacgttggtgtgtcatttgtctgtcctagtggtggttagag	60
OY	101	acaagaatcatctgcagatctcctgttagtaactgccagctgtgacatctctgtatataac	160
Db	61	gtgggagccgtctgcagaaactcctgtgataactgttcaagcctgttaacttctgcgaataac	120
OY	161	aggaatcgaatttgcagttccctgtctctccaataagtcttccagcgcaggttgacaag	220
Db	121	--aatccagttctgcaagagctgtccctccaagtactcttccagcataggtgtgacagcg	177
OY	221	accttgcacatctgcagcgaagtgtaaagttgttttttttttccaggaagagtgctctcc	280
Db	178	aactgttaacatctgcagagtggtgtgcgcagctatlttaagttcaagaagtttgcctctt	237
OY	281	accagcaatgcagagtggtgacgtcacctccagagtttcaactgtctgtgggcagagatcagc	340
Db	238	accacaagaacgagtggtgtgagtgcatgtgaaggtatccattgtctgtgggcacacagtgacc	297
OY	341	atgtgtgaacagagattgttaaacaaagttcaagaactgtgacaaaaaaggtgtgtaaagact	400
Db	298	agatgtgaagaagactgcagcgctgtgccagagctaacgaagaacagaggtgtgcaaaaactgt	357
OY	401	tgcttgggacatttaacgatcatgaagaag---tgcatctgtgcagccctgggcaaatgt	457
Db	358	agcttggggaactcttaatgtaccagaacaggtactgtggtctgtctgcagccctgggacgaactgc	417
OY	458	tcttggatgataagctctgtgtctgttgaaatggagacgaagagagagactgtgtctgtga	517
Db	418	tctctagaacggaaggtctgtgtcttaagaacgggacacgaagaaaggaagctgtgtgtgtga	477
OY	518	caatctcaagctgaactctctctccgggagagatcctgtgtgaccccgctgcacctgtgaa	577
Db	478	cccctgtgtgtgagcttctctccag---taccacattctgtgatactccagagggagga	534
OY	578	gagcagagaacactctccgagatacatctctcttctgtgcgtcagctgcagctgcgtg	637
Db	535	ccagagaggaacactcctctccaggttccattactgttctctgcgtccataacacg---cttgg	591

```

QY 638 ctcttcgtgtcttcttcacgctccgttctctgttgaacgggagagaaga 697
   || || || || || || || || || || || || || || || || || ||
Db 592 ctgttgccctgattcattcattctctctctctgtctgtcctaattgataagaaaa 651
QY 698 ctctgtatattatcaacaacattatagagaccagttacaactactcaagaagaagat 757
   || || || || || || || || || || || || || || || || || ||
Db 652 ttcccccaatttcaagaacatttaagaagacgtgagagctcacaagaagaagat 711
QY 758 ggcgtgagcgcgatttccagaagaagaagaagagatgtgaa 802
   || || || || || || || || || || || || || || || || || ||
Db 712 gctgtgagcgcgatttccagaagaagaagaagaagaagaaga 756

RESULT 15
V62467
ID V62467 standard; cDNA; 2781 BP.
AC V62467;
XX
DE 21-JAN-1999 (first entry)
XX
XX Human dendritic cell receptor protein encoding cDNA.
XX
XX Receptor protein; ligand: therapeutic agent; breast cancer; AIDS;
KM prostate cancer; ovarian cancer; follicular lymphoma; p53 mutation;
KM brain tumour; bladder carcinoma; cervical cancer; intestinal cancer;
KM lung cancer; gastric cancer; herpesvirus; adenovirus; human;
KM H. pylori infection; varicella-zoster virus; human papillomavirus;
KM staphylococcal; influenza virus; systemic mycosis; bacterial pneumonia;
KM bacterial peritonitis; viral encephalitis; diabetes mellitus; sepsis;
KM adult respiratory distress syndrome; leukaemia; malignant melanoma;
KM multiple myeloma; non-Hodgkin lymphoma; peptic ulcer; septic shock;
KM tuberculosis; immunological disease; dermatitis; allergic rhinitis;
KM pollen allergy; inflammation; arthritis; hepatitis; autoimmune disease;
KM rheumatoid arthritis; disseminated lupus erythematosus; bronchial asthma;
KM Sjogren's disease; glomerulonephritis; ss.
XX
XX Homo sapiens.
XX
XX OS
XX FH
XX Key Location/Qualifiers
XX FT sig_peptide 19..105
XX FT CDS /tag= a
XX FT 19..1869
XX FT /tag= b
XX FT /product= "receptor protein"
XX FT /tag= c
XX FT /note= "sequence coding for a partial soluble peptide"
XX FT mat_peptide 106..1866
XX FT /tag= d
XX
XX EP873998-A2.
XX
XX 28-OCT-1998.
XX
XX PF 24-APR-1998; 98EP-0303190.
XX
XX 17-SEP-1997; 97JP-0251867.
XX
XX 25-APR-1997; 97JP-0109798.
XX
XX (TAKE ) TAKEDA CHEM IND LTD.
XX
XX Horiguchi T, Nishi K, Shintani A;
XX
XX WPI: 1998-544608/47.
XX
XX P-PSDB; W79233.
XX
XX New dendritic cell receptor belonging to TNF receptor family - used
XX to treat e.g. cancer, AIDS, bacterial and viral infections,
XX insulin-dependent diabetes mellitus, peptic ulcer, sepsis, septic
XX shock and allergic immunological disorders
XX

```

```

PS Disclosure: Fig 1; 65pp; English.
XX
CC This represents the nucleotide sequence of a receptor protein derived
CC from a human dendritic cell. The receptor protein or its fragment or
CC salt can be used to determine a ligand to it, and for screening a
CC compound which alters binding properties between it and a ligand. The
CC compound is used for therapeutic purposes. The therapeutic agents are
CC used to treat cancer (breast cancer, prostate cancer, ovarian cancer,
CC follicular lymphoma, cancer accompanied by p53 mutation, brain tumour,
CC bladder carcinoma, cancer of uterine cervix, cancer of large intestine
CC (carcinoma of colon and rectum), non-small and small cell lung cancer
CC and gastric cancer), AIDS, infections (e.g. herpesvirus, adenovirus,
CC poxvirus, H. pylori, varicella-zoster virus, human papillomavirus,
CC active), staphylococcal and influenza virus infections and severe systemic
CC mycosis), acute bacterial peritonitis, acute viral encephalitis, adult
CC respiratory distress syndrome, bacterial pneumonia, chronic lymphocytic
CC leukaemia, chronic myelogenous leukaemia, insulin-dependent diabetes
CC mellitus (type 1), malignant melanoma, multiple myeloma, non-Hodgkin
CC lymphoma, peptic ulcer, sepsis, septic shock, tuberculosis, allergic
CC immunological diseases (e.g. atopic dermatitis, contact dermatitis,
CC allergic rhinitis and pollen allergy), inflammation (e.g. arthritis and
CC hepatitis), autoimmune diseases (e.g. rheumatoid arthritis, disseminated
CC lupus erythematosus and Sjogren's disease), glomerulonephritis and
CC bronchial asthma.
XX
SQ Sequence 2781 BP; 585 A; 811 C; 778 G; 607 T; 0 other.

Query Match 4.3%; Score 36.4; DB 19; Length 2781;
Best Local Similarity 61.7%; Pred. No. 0.2;
Matches 58; Conservative 0; Mismatches 36; Indels 0; Gaps 0;
QY 431 ggcattctgcaccctgacaaactgtcttctgagagaagctgtgtgaaatgg 490
   || || || || || || || || || || || || || || || || || ||
Db 517 gacaaatgcagaccctgacccaactgtactctctctggaagaagatgaacatcatgg 576
QY 491 acgaagagagagagcgtgtgtctgtgaccatctc 524
   || || || || || || || || || || || || || || || || || ||
Db 577 acagagaatcgcattgtgtgtgagctctctc 610

```

Search completed: November 22, 2000, 05:34:24
Job time: 6883 sec

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: November 22, 2000, 00:49:40 ; Search time 61.81 Seconds
(Without alignments)
2050.483 Million cell updates/sec

Title: US-08-955-572-1

Sequence: 1 aatcagcttgcctagatca.....aataggctgttggaactt 838

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Gapop 10.0 , Gapext 1.0

Searched: 262060 seqs, 75620727 residues

Total number of hits satisfying chosen parameters: 524120

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents.NA.*

1: /cgn2_6/prodata/2/lna/5A_COMB.seq:*
2: /cgn2_6/prodata/2/lna/5B_COMB.seq:*
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6: /cgn2_6/prodata/2/lna/PCrus_COMB.seq:*
7: /cgn2_6/prodata/2/lna/Backfilseq1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	838	100.0	838	6	PCT-US94-10457-1
2	838	100.0	838	6	PCT-US96-03965-7
3	836.4	99.8	1415	1	US-08-236-918A-7
4	608.8	72.6	946	3	US-08-816-605-1
5	339.2	40.5	2347	6	PCT-US96-03965-1
6	331.4	39.5	768	1	US-08-236-918A-5
7	45.6	5.4	7218	1	US-08-232-463-14
8	42.2	5.0	7218	1	US-08-232-463-14
9	35.8	4.3	3133	1	US-08-162-809-1
10	34.8	4.2	1391	5	US-08-996-139-3
11	34.8	4.2	3115	5	US-08-996-139-1
12	34.8	4.2	3136	5	US-08-996-139-5
13	32	3.8	723	5	US-08-911-423-5
14	31.4	3.7	15231	5	US-09-128-155-16
15	31.4	3.7	176373	5	US-09-128-155-17
16	31	3.7	4060	1	US-08-308-949A-1
17	31	3.7	246240	3	US-08-724-394A-20
18	31	3.7	246240	3	US-08-724-394A-21
19	31	3.7	246240	3	US-08-724-394A-22
20	30.6	3.7	291	1	US-07-922-723A-7
21	30.6	3.7	291	1	US-07-922-723A-7
22	30.6	3.7	291	1	US-08-074-275-7
23	30.6	3.7	291	2	US-08-480-366-7
24	30.6	3.7	291	2	US-07-952-277A-7
25	30.4	3.6	12127	5	US-08-444-644-32
26	30	3.6	30	4	US-08-859-998-420

27	29.6	3.5	6256	3	US-08-475-891A-1	Sequence 1, Appl
28	29.6	3.5	6256	4	US-08-567-375-1	Sequence 1, Appl
29	29.6	3.5	6256	4	US-08-587-680A-1	Sequence 1, Appl
30	29.4	3.5	3918	5	US-08-836-329-1	Sequence 1, Appl
31	29.2	3.5	363	4	US-08-966-316-8	Sequence 8, Appl
32	29	3.5	1558	2	US-08-487-823B-1	Sequence 1, Appl
33	29	3.5	1558	4	US-08-997-040-1	Sequence 1, Appl
34	29	3.5	1558	4	US-09-203-237-1	Sequence 1, Appl
35	29	3.5	1564	5	US-08-948-997-1	Sequence 1, Appl
36	28.8	3.4	2652	3	US-08-766-738-2	Sequence 1, Appl
37	28.8	3.4	2652	3	US-08-366-547-1	Sequence 1, Appl
38	28.6	3.4	519	4	US-08-249-189-4	Sequence 4, Appl
39	28.6	3.4	519	4	US-08-464-624A-4	Sequence 4, Appl
40	28.6	3.4	519	4	US-08-477-733B-4	Sequence 4, Appl
41	28.6	3.4	519	5	US-09-088-913A-4	Sequence 4, Appl
42	28.6	3.4	1318	2	US-08-419-009-27	Sequence 27, Appl
43	28.6	3.4	1358	2	US-08-419-009-29	Sequence 29, Appl
44	28.6	3.4	1436	2	US-08-419-009-28	Sequence 28, Appl
45	28.6	3.4	1435	2	US-08-419-009-26	Sequence 26, Appl

ALIGNMENTS

RESULT 1
PCT-US94-10457-1
Sequence 1, Application PC/TUS9410457
GENERAL INFORMATION:
APPLICANT: Byong Se Kwon
TITLE OF INVENTION: New Human Receptor and Related Products
TITLE OF INVENTION: and Methods
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Barnard & Brown
STREET: 306 E. State St., Suite 220
CITY: Ithaca
STATE: New York
COUNTRY: United States
ZIP: 14850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: IBM AT Compatible
OPERATING SYSTEM: MS DOS, Version 5.0
SOFTWARE: Special Basic program
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/10457
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/012,269
FILING DATE: 2/1/93
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/922,996
FILING DATE: 7/30/92
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/267,577
FILING DATE: 11/7/88
ATTORNEY/AGENT INFORMATION:
NAME: Michaels, Christopher A.
REGISTRATION NUMBER: 34,350
REFERENCE/DOCKET NUMBER: kmh41db
TELECOMMUNICATION INFORMATION:
TELEPHONE: 607-273-1711
TELEFAX: 607-273-2609
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 838
TYPE: nucleic acid
STRANDEDNESS: double stranded
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO


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? TOPOLOGY: linear
? MOLECULE TYPE: cDNA to mRNA
? HYPOTHETICAL: NO
? ANTI-SENSE: NO
? ORIGINAL SOURCE:
? ORGANISM: Homo sapiens
? INDIVIDUAL ISOLATE: H4-1B8 #1
? DEVELOPMENTAL STAGE: Differentiated T-cell
? CELL TYPE: Lymphocyte
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 41..805
? OTHER INFORMATION: /codon_start= 41
? OTHER INFORMATION: /product= "H4-1B8"
? OTHER INFORMATION: /number= 1
? FEATURE:
? NAME/KEY: mat_peptide
? LOCATION: 41..802
? OTHER INFORMATION: /codon_start= 41
? OTHER INFORMATION: /product= "H4-1B8"
? OTHER INFORMATION: /number= 1
PCT-US96-03965-7

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Best Local Similarity 100.0%; Pred. No. 9.7e-251;
Matches 838; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 aatcagcttctagatcatatccctgtgccaagattcatcatcaggaaacagctgttcaaa 60
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Db 1 AATCAGCTTTGCTAGTATCATCTGTCGCCAGATTTCATCATGGAAACAGCTTTTCAA 60

QY 61 catagtgcacatctgttctgtcctcaacttgaggagacaagatcatctgcagatcc 120
   |||||
Db 61 CATAGTAGCCACTGTGTCTGCTGCTCAACTTTGAGAGACAAGATCATTTGCAGATCC 120

QY 121 tttaagtaactgcccagctgtgtacattctgtgataatacaagaaatagatttgcattcc 180
   |||||
Db 121 TTGAGTAGTAAGTCCGACCTGCTGATCATTTGATTAACAGGAATGAGATTGCCAGTCC 180

QY 181 ctgtccctcaaatagtttccacagcaggctgagcaaaagaccctgtacatatgcagca 240
   |||||
Db 181 CTGTCCCTCAAAATAGTTTCTCCAGCGCAGGTGGCAAAAGACCTGTACATATGCAGCA 240

QY 241 ggttaagagtgcttcaagagcaagaaagagtgcttccctcacaagaatgcagagtgta 300
   |||||
Db 241 GGTAAAGGTGTTTTCAGGACCAAGAGAGAGTGTCTCCACCAAGCAATGCAGAGTGTGA 300

QY 301 ctgcactccaggggtttcactgcctgtgggagagatgtagcatgtgtgaaagaattgtaa 360
   |||||
Db 301 CTGCACCTCCAGGGGTTTCTACTGCTGGGGGCAAGATGCAGATGTGTAACAGGATTTGAA 360

QY 361 acaaggtcaagaactgcagaaaaaaggctgtgaaagactgttcttggagcaattaaaga 420
   |||||
Db 361 ACAAGGTCAAGAACTGCAGAAAAAAGGTGTGTAAGACTGTTCCTTTGGGACATTTAACA 420

QY 421 tcagaaacgtgtgacatctgtgcaccctggacaacactgttcttggatgaaagtcgtgct 480
   |||||
Db 421 TCAGAAACGTGGCATCTGTGCACCTTGACAAACTGTTCTTTGGATGAAAGTCGTGCT 480

QY 481 tctgaatggagaaagagagagagagctgtgtgtgagccatctccagctcactctcc 540
   |||||
Db 481 TCTGAATGGAGAGAGAGAGAGAGCTGTGTGTGGACCATCTCCACCTCCTCTCC 540

QY 541 gggagcatccctctgtgaccccgctgcccctgcagagagacagaaacactccagat 600
   |||||
Db 541 GGGAGCATCCTCTGTGACCCCGCTGCCCTCGCAGAGAGACCAAGACACTCCGCGAGAT 600

QY 601 catctcccttcttctgtgagctgagcgtgcagctgctgtcttccctgttcttccac 660
   |||||
Db 601 CATCTCCCTTCTTCTGTGAGCTGAGCTGACGTCGACTGCGTTCTCTCTGCTGTTCTTCAC 660

QY 661 gctcgccttctctgtgtttaaacygggcagaaagaacactccgtatataatcaacaac 720
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Db 661 GCTCGTTTCTCTGTTGTTAAACGGGCGAAGAAACTCCTGTATATTCAAAACACC 720

QY 721 attatgagaccagttacaactactcaagagaaagatgctgtagctgcgattccaga 780
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Db 721 ATTATGAGACCAGTACAAACTACTCAAGAGAAAGATGCTGTAGCTGCCATTTCCAGA 780

QY 781 agaaagaagaagagatgtgaactgtgaaatggaagtcataagggctgttggacctt 838
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Db 781 AGAAGAAGAAGAGAGATGTGAATGTAATGCAATGCAATAGGCGCTGTGCACTTT 838

RESULT 3
US-08-236-918A-7
? Sequence 7, Application US/08236918A
? Patent No. 5674704
? GENERAL INFORMATION:
? APPLICANT: Alderson, Mark R.
? APPLICANT: Goodwin, Raymond G.
? APPLICANT: Smith, Craig A.
? TITLE OF INVENTION: Cytokine Designated 4-1BB Ligand
? NUMBER OF SEQUENCES: 18
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
? STREET: 51 University Street
? CITY: Seattle
? STATE: Washington
? COUNTRY: US
? ZIP: 98101
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? OPERATING SYSTEM: Apple Power Macintosh
? SOFTWARE: Microsoft Word, Version #6.0.1
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/236,918A
? FILING DATE: 06-May-1994
? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/060,843
? FILING DATE: 07-May-1993
? CLASSIFICATION: 435
? ATTORNEY/AGENT INFORMATION:
? NAME: Anderson, Kathryn A.
? REGISTRATION NUMBER: 32,172
? REFERENCE/DOCKET NUMBER: 2801-B
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (206) 587-0430
? TELEFAX: (206) 233-0644
? INFORMATION FOR SEQ ID NO: 7:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1415 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: cDNA to mRNA
? HYPOTHETICAL: NO
? ANTI-SENSE: NO
? IMMEDIATE SOURCE:
? CLONE: hu4-1B8
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 120..887
? FEATURE:
? NAME/KEY: mat_peptide
? LOCATION: 189..884
? FEATURE:
? NAME/KEY: sig_peptide
? LOCATION: 120..188
US-08-236-918A-7

Query Match      99.8%; Score 836.4; DB 1; Length 1415;
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Best Local Similarity 99.9%; Pred. No. 4e-250;
Matches 837; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 aatgaagcttgcgtatcatatcaccgtgctccagattctcatctggaagaacagctgttaca 60
Db 80 AATGAGCTTTGCTATATCATATCATCTGTCGCAATTCATCAGGAAACAGCTGTATACA 139
QY 61 catagtaacacactgtgtgctgctcactcttagaggaacaatcatatcagaatcc 120
Db 140 CATAGTACCACTGCTGTGCTGCTCTCACTTTAGAGGACAAATCATCTTCAGAGATCC 199
QY 121 ttgtagtaactgcccagctggtaactctgtgataataacaaggaatcagatttgatcc 180
Db 200 TTGTAGTAGTAACTGCCAGCTGGTACATCTGTGATTAATAACAGAGATTCAGATTGCCAGTCC 259
QY 181 ctgtccctcaaatagttcttccagcagagtggaacaaggacctgtgacatctgcaagca 240
Db 260 CTGTCTCTCAATATATATTTCTCCAGCGAGGTGACAAAGAGACCTGTGACATTCAGAGCA 319
QY 241 gtgtaaaggtgttttcaagaccagaagaagagtgcttccctccacaagaatgcaagtgta 300
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QY 301 ctgcactccaggggttcaactgctggggcaggaatgcagcatgtgtgaacaggaattgtaa 360
Db 380 CTGCACCTCCAGGGGTTCACCTGCTGGGGCAGGATGACAGCATGTGTGAACAGGATTTGTAA 439
QY 361 acaaggtcaagaagactgacaaaaaaggtgtgaagaactgtgtgcttggagactttaagca 420
Db 440 ACAAGGTCAAGAAGACTGACAAAAAAGTTGTAAAGACTGTGCTTTGGACATTTAAACCA 499
QY 421 tcagaagaactgcatctgtcgaaccttgacaacactgtcttcttgaatggaatctgtgct 480
Db 500 TCAGAAGACTGGCATCTGTGACACCTGAGCAAACTGTTCTTTGATGGAATGCTGTGCT 559
QY 481 ttgtgaatggagaaaggaaggaaggaagtgctgtgtgagacatctccagctgacatctctcc 540
Db 560 TGTGAATGGGAGGAGAGGAGGAGGAGTGTGTGTGACCATCTCCAGCGACCTCTCTCC 619
QY 541 gggagacatccctgtgagaccgcccgtccgcctggaagagacaggaacactcccgcaat 600
Db 620 GGGAGACATCCCTGTGACCCGCCCTGCCCCGAGAGAGGCCAGACACTCTCCCGAGAT 679
QY 601 catctcctcttctctgtgctgacgtcgaactgctgtctctctccctgcttctccac 660
Db 680 CATCTCCTTCTTCTTGTGGCTGAGCTGCAGCTGCTGCTCTCCGCTCTTCTCTCCAC 739
QY 661 gctccgttctctgtgtttaaaggggagagaagaactcctgtatataattcaaaacac 720
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Db 800 ATTATGTAGACCACTACAACTACTCAAGAGAAATGGCTGTACTGCGGATTTCCAGA 859
QY 781 agaagaagaagaagatgtgaactgtgaatggaagtcataagggctgttggaacttt 838
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RESULT 4
US-08-816-605-1
Sequence 1, Application US/08816605
Patent No. 5874240

GENERAL INFORMATION:
APPLICANT: NI, Jian
APPLICANT: Yu, Guo-Liang
APPLICANT: Gentz, Reiner
TITLE OF INVENTION: Human 4-1BB Receptor Splicing Variant
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue

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/? CITY: Rockville
/? STATE: MD
/? COUNTRY: USA
/? ZIP: 20850
/? COMPUTER READABLE FORM:
/? MEDIUM TYPE: Floppy disk
/? OPERATING SYSTEM: PC-DOS/MS-DOS
/? SOFTWARE: Patent Release #1.0, Version #1.30
/? CURRENT APPLICATION DATA: US/08/816, 605
/? APPLICATION NUMBER:
/? FILING DATE: 13-MAR-1997
/? CLASSIFICATION: 435
/? ATTORNEY/AGENT INFORMATION:
/? NAME: Brookes, A. Anders
/? REGISTRATION NUMBER: 36, 373
/? REFERENCE/DOCKET NUMBER: PF254
/? TELECOMMUNICATION INFORMATION:
/? TELEPHONE: 301-309-8512
/? TELEFAX: 301-309-8504
/? INFORMATION FOR SEQ ID NO: 1:
/? SEQUENCE CHARACTERISTICS:
/? LENGTH: 946 base pairs
/? TYPE: nucleic acid
/? STRANDEDNESS: single
/? TOPOLOGY: linear
/? MOLECULE TYPE: DNA (genomic)
/? FEATURE:
/? NAME/KEY: CDS
/? LOCATION: 124..780
/? FEATURE:
/? NAME/KEY: sig_peptide
/? LOCATION: 124..177
/? FEATURE:
/? NAME/KEY: mat_peptide
/? LOCATION: 178..780
/? US-08-816-605-1
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Best Local Similarity 86.9%; Pred. No. 1.5e-179;
Matches 728; Conservative 0; Mismatches 2; Indels 108; Gaps 1;

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QY 61 catagtaacacactgtgtgctgctcactcttagaggaacaatcatatcagaatcc 120
Db 144 CATAGTACCACTGCTGTGCTGCTCTCACTTTAGAGGACAAATCATCTTCAGAGATCC 203
QY 121 ttgtagtaactgcccagctggtaactctgtgataataacaaggaatcagatttgatcc 180
Db 204 TTGTAGTAGTAACTGCCAGCT----- 222
QY 181 ctgtccctcaaatagttcttccagcaggtggaacaaggacctgtgacatctgcaagca 240
Db 223 ----- 222
QY 241 gtgtaaaggtgttttcaagaccagaagaagtgcttccctccacaagaatgcaagtgta 300
Db 223 -----GGTGTTCACAGACCCAGGAAGAGGTTCCTCCACACAGCAATGACAGATGTGA 275
QY 301 ctgcactccaggggttcaactgctctggggcaggaatgcaagcatgtgtgaacaggaattgtaa 360
Db 276 CTGCACCTCCAGGGGTTCACCTGCTGGGGCAGAGATGCACATGTGTGAACAGGATTTGTAA 335
QY 361 acaaggtcaagaagactgacaaaaaaggtgtgaagaactgtgttggagactttaagca 420
Db 336 ACAAGGTCAAGAAGACTGACAAAAAAGGTGTGAAGACTGTGCTTTGGACATTTAAACA 395
QY 421 tcagaagaactgcatctgtcgaacctggaacaactgttcttgagatggaatctgtgct 480
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	LENGTH: 2347 base pairs
	TYPE: nucleic acid
	STRANDEDNESS: single
	TOPOLOGY: linear
	MOLECULE TYPE: cDNA to mRNA
	ORIGINAL SOURCE:
	ORGANISM: murine 4-1BB
FEATURE:	
NAME/KEY: CDS	
LOCATION: 146..916	
FEATURE:	
NAME/KEY: mat_peptide	
LOCATION: 146..913	
PUBLICATION INFORMATION:	
AUTHORS: Kwon, Byoung Se	
AUTHORS: et al.,	
TITLE: cDNA sequences of two inducible T-cell genes	
JOURNAL: Proc. Natl. Acad. Sci. U.S.A.	
VOLUME: 86	
ISSUE: March	
PAGES: 1963-1967	
DATE: 1989	
RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 2347	
PCT-US96-03965-1	
Query Match	40.5%; Score 339.2; DB: 6; Length 2347;
Best Local Similarity	67.8%; Pred. No. 1.3e-95;
Matches 537; Conservative 0; Mismatches 243; Indels 12; Gaps	
QY 14	agatcatcaccgtgycagatattcatcatggyaaacagctgtltaacaatagtagccact 73
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QY 74	ctgtgtcgtgtccccaactttgagaggaacaagatcatcgaggaacctttagtaactgc 133
DB 179	GTCGTGCTGCTAGTGGGGCTGTGAGAAAGGTGGAGCCGTCGAGAACTCCTGTGATMACTGT 236
QY 134	ccagctgtatcatctctgtgataataaagagatcagatttgcagctccctgtccccaat 199
DB 239	CAGCCTGTGATCTTCTGACAGAAATATC--AATCCAGCTGCTCAAGAGACTGACCTGTCAGAT 299
QY 194	agttctcccaagcaggtgtgacaagaagacctgtacatatgcagcaggttgaaggtgt 253
DB 296	ACCTTCTCCACACATAGTGTGAGACCCGACACTGTAACTCTCCAGATGTGTGACAGCTAT 355
QY 254	ttcagaccaggaagagtgcttctccacacagcaatgcagagtgtagctgcactccaggg 313
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QY 314	tttaccgtccctgggggagagatgtgaagcatgtgtgaacaagatgtgtaacaaggtcgaag 373
DB 416	TTTCATTGCTTTGGGGCCACACTGTCACACAGAGTGAATAAAGGCTGACAGCCCTGGCCAGAG 475
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DB 476	CTAACGAAGACGGGTTGCAAAACCTGTAGCTTGGGAACATTTAATGACACAGAGGTAAT 533
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DB 536	GGCGTCTGTGTGACCCCTGGACGAATGCTCTGTAGACGGAAGGTGTGTGCTTAAGACCGGG 599
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DB 596	ACCCAGGAAGAGCGTGTGTGTGGACCCCTGTGTGAGCTTCTTCCAG--TACC 652
QY 551	tctgtgaccccgccctgtccctctcgagagagcaaggaacactctccgagatcatctcttc 610
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QY 611	ttctctgcctgtagctgcagactcgtgtctctctctctgtcttctctcccaagctcgttctc 670
DB 713	TTCTGCGCGGTGAATG---GCTTGTGCTGTGGCCCTGATATCATTAATCTGCTGTTG 769


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? COUNTRY: USA
? ZIP: 22313-0299
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/232,463
? FILING DATE:
? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US/07/935,313
? FILING DATE:
? APPLICATION NUMBER: EP 91 114 300.6
? FILING DATE: 26-AUG-1991
? ATTORNEY/AGENT INFORMATION:
? NAME: BENT, Stephen A.
? REGISTRATION NUMBER: 29,768
? REFERENCE/DOCKET NUMBER: 30472/114 IMMU
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (703)836-9300
? TELEFAX: (703)683-4109
? TELEX: 899149
? INFORMATION FOR SEQ ID NO: 14:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 7218 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? IMMEDIATE SOURCE:
? CLONE: PTZgpt-F15
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US-08-232-463-14

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Query Match          5.4%; Score 45.6; DB 1; Length 7218;
Best Local Similarity 10.0%; Pred. No. 0.00033;
Matches 21; Conservative 115; Mismatches 74; Indels 0; Gaps 0;

QY 470 aagctcgtctgtgaatggaagagagagagctgtctgtgacatctccagct 529
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DB 1029 AATTCGACCTTGCTGCGAGGTCGAGGAGCTTGCGATYYYYYYYYYYYYYY 1088
QY 530 gacctctccgaggacatctgtgacccgcctgcccctgagagagccagacac 589
    : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1089 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1148
QY 590 tcttcgcagatcatctctcttctctgctgagctgacgtcgctctctcgtcg 649
    : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1149 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1208
QY 650 tcttcctcagcgtccgtctctctgtgt 679
    : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1209 YYYYYYYYYYYYYYYYYYYYYYYYYY 1238

RESULT 8
US-08-232-463-14/C
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299

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? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/232,463
? FILING DATE:
? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US/07/935,313
? FILING DATE:
? APPLICATION NUMBER: EP 91 114 300.6
? FILING DATE: 26-AUG-1991
? ATTORNEY/AGENT INFORMATION:
? NAME: BENT, Stephen A.
? REGISTRATION NUMBER: 29,768
? REFERENCE/DOCKET NUMBER: 30472/114 IMMU
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (703)836-9300
? TELEFAX: (703)683-4109
? TELEX: 899149
? INFORMATION FOR SEQ ID NO: 14:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 7218 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? IMMEDIATE SOURCE:
? CLONE: PTZgpt-F15
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US-08-232-463-14

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RESULT 9
US-08-162-809-1
; Sequence 1, Application US/08162809
; Patent No. 5457048
; GENERAL INFORMATION:
; APPLICANT: Pasquale, Elena B.
; APPLICANT: Sajjadi, Fereydon G.
; TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES,
; NUCLEOTIDE SEQUENCES, AND METHODS OF USE
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:

```



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1 MEDIUM TYPE: Floppy disk
2 COMPUTER: Apple Power Macintosh
3 OPERATING SYSTEM: Apple Operating System 7.5.5
4 SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
5 CURRENT APPLICATION DATA:
6 APPLICATION NUMBER: US/08/996,139
7 FILING DATE: 22 DECEMBER 1997
8 CLASSIFICATION:
9 PRIOR APPLICATION DATA:
10 APPLICATION NUMBER: USSN 60/064,671
11 FILING DATE: 14 OCTOBER 1997
12 PRIOR APPLICATION DATA:
13 APPLICATION NUMBER: USSN 08/813,509
14 FILING DATE: 07 MARCH 1997
15 PRIOR APPLICATION DATA:
16 APPLICATION NUMBER: USSN 08/772,330
17 FILING DATE: 23 DECEMBER 1996
18 ATTORNEY/AGENT INFORMATION:
19 NAME: Perkins, Patricia Anne
20 REGISTRATION NUMBER: 34,693
21 REFERENCE/DOCKET NUMBER: 2851-A
22 TELECOMMUNICATION INFORMATION:
23 TELEPHONE: (206)233-0644
24 TELEFAX: (206)587-0430
25 INFORMATION FOR SEQ ID NO: 5:
26 SEQUENCE CHARACTERISTICS:
27 LENGTH: 3136 base pairs
28 TYPE: nucleic acid
29 STRANDEDNESS: single
30 TOPOLOGY: linear
31 MOLECULE TYPE: CDNA
32 HYPOTHEICAL: NO
33 ANTI-SENSE: NO
34 ORIGINAL SOURCE:
35 ORGANISM: HOMO SAPIENS
36 IMMEDIATE SOURCE:
37 LIBRARY: BONE-MARROW DERIVED DENDRITIC CELLS
38 CLONE: FULL LENGTH RANK
39 FEATURE:
40 NAME/KEY: CDS
41 LOCATION: 39..1886
42 US-08-996-139-5
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44 Query Match 4.2%; Score 34.8; DB 5; Length 3136;
45 Best Local Similarity 60.6%; Pred. No.0.49;
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50 Db 537 GACAAATGTCAGACCCCTTGACCAACTGTACCTTCCTTGGAAAGAGTAAACATCATGCG 596
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52 QY 491 acgaagagagagagacgtgtgtctgttgaccatc 524
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54 Db 597 ACAGAGAAATCCGATGCGGTTTGACAGTCTTCTC 630
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56 RESULT 13
57 US-08-911-423-5
58 ; Sequence 5, Application US/08911423
59 ; Patent No. 6111090
60 ; GENERAL INFORMATION:
61 ; APPLICANT: Gorman, Daniel M.
62 ; APPLICANT: Randall, Troy D.
63 ; APPLICANT: Zlotnick, Albert
64 ; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
65 ; NUMBER OF SEQUENCES: 8
66 ; CORRESPONDENCE ADDRESS:
67 ; ADDRESSEE: DNAX Research Institute
68 ; STREET: 901 California Avenue
69 ; CITY: Palo Alto
70 ; STATE: California
71 ;

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Fri Nov 24 17:29:10 2000

us-08-955-572-1.rni

Page 11

Db 38794 gcactcgtatctactccttcttcttaatgac 38822

Search completed: November 22, 2000, 05:34:18
Job time: 17078 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 22, 2000, 00:29:20 ; Search time 770.21 Seconds

(without alignments)
6726.986 Million cell updates/sec

Title: US-08-955-572-1

Perfect score: 838
Sequence: 1 aatcaagcttgctagtatca.....aataggcctgttggaactt 838

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7189864 segs, 3091403243 residues

-Total number of hits satisfying chosen parameters: 14379728

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

-Post-processing: Minimum Match 08

Maximum Match 1008
Listing first 45 summaries

Database :

EST:*

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2: gb_est2:*
3: gb_est3:*
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116: em_gss5:*

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124: em_gss13:*
125: em_gss14:*
126: em_gss15:*
127: em_gss16:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	491	58.6	570	BE207340	BE207340 ba85f11.y
2	272	32.5	548	BE233113	BE233113 139153 MA
3	241	28.8	630	AA109726	AA109726 mp10f11.r
4	235.2	28.1	667	AI236084	AI236084 EST232646
5	231	27.6	674	AA946462	AA946462 EST201961
6	203.2	24.2	589	AA087107	AA087107 mol3901.r
7	198.6	23.7	491	AI664286	AI664286 ue83005.r
8	79.8	9.5	332	AI172529	AI172529 UT-R-C2P-
9	58.6	7.0	330	AW920027	AW920027 EST35131
10	57.4	6.8	291	AI555584	AI555584 UT-R-C2P-
11	42.4	5.1	688	AA166859	AA166859 zq41c02.s
12	40.2	4.8	578	AA618624	AA618624 np38h10.s
13	39.8	4.7	529	N80901	N80901 zb07b08.s1
14	38.8	4.6	304	BB290438	BB290438 BB290438
15	38	4.5	468	AA0933674	AA0933674 RPT-23-2
16	38	4.5	573	AA0205913	AA0205913 RPT-23-3
17	37.8	4.5	748	AZ228414	AZ228414 RPT-23-7
18	37.6	4.5	383	AA0722028	AA0722028 HS_3020.A
19	36.6	4.4	803	AA109287	AA109287 Drosophill
20	36.2	4.3	404	AW746620	AW746620 WSL_54_F0
21	36.2	4.3	442	AA775053	AA775053 ac76103.s
22	36	4.3	751	AA0869200	AA0869200 nbe600341
23	36	4.3	1101	CNS01784	AL107710 Drosophill
24	35.8	4.3	382	AA796144	AA796144 MR2-UM002
25	35.8	4.3	676	AZ276416	AZ276416 RPT-23-1
26	35.6	4.2	291	BB232607	BB232607 BB232607
27	35.6	4.2	430	BE524618	BE524618 NS2B9STM
28	35.4	4.2	904	AZ208857	AZ208857 SP_0152_A
29	35.4	4.2	1068	AL489746	AL489746 Tetraodon
30	35.2	4.2	417	AW146746	AW146746 614083B05
31	35.2	4.2	504	AA0785579	AA0785579 HS_3077.A
32	35	4.2	375	AW157881	AW157881 D05 Neosp
33	35	4.2	459	CNS03610	AL424243 Tetraodon
34	35	4.2	1101	CNS012RM	AL101932 Drosophill
35	35	4.2	1101	CNS016N6	AL106956 Drosophill
36	35	4.2	1201	CNS01638	AL106228 Drosophill
37	34.8	4.2	261	BB324451	BB324451 BB324451
38	34.8	4.2	424	AA0218065	AA0218065 HS_3251.B
39	34.8	4.2	561	AA0391329	AA0391329 QV0-ST021
40	34.8	4.2	562	AA0380345	AA0380345 QV3-HT026
41	34.6	4.1	751	AZ200704	AZ200704 SP_1026.A
42	34.6	4.1	505	AA613256	AA613256 no19h02.s
43	34.6	4.1	679	AA0795961	AA0795961 nbx000587
44	34.6	4.1	1101	CNS006BP	AL064052 Drosophill
45	34.4	4.1	287	AA310664	AA310664 EST181611

ALIGNMENTS

RESULT 1
BE207340

LOCUS	BE207340	570 bp	mRNA	EST	27-JUN-2000
DEFINITION	ba85f11.y1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2924109 5' similar to gb:J04492 Mouse T-cell receptor 4-1BB protein mRNA, complete cds (mouse), mRNA sequence.				
ACCESSION	BE207340				
VERSION	BE207340.1	GI:8750738			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	1 (bases 1 to 570)				
TITLE	NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/				
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)				
COMMENT	Unpublished (1999) Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email: Robert_Strausberg@nih.gov Tissue Procurement: DCTD/DTP CDNA Library Preparation: Ling Hong/Rubin Laboratory DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/MLN at: image.lnl.gov/image/html/lresources.shtml Seq primer: -40RP from Gldco High quality sequence stop: 516.				
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source	1..570 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:2924109" /clone_lib="NIH_MGC_14" /tissue_type="renal cell adenocarcinoma" /lab_host="DH10B (phage-resistant)" /note="Organ: kidney; Vector: pOT7; Site:1: XhoI; Site:2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAC(G). Size selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."				
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QY	61	catagtagcacctcgttcgtcgttcctcaactctgagaggaacaagatcagagatcc	120		
DB	140	CATAGTAGCACCTCGTTCGTGTCCTCAACTTTCAGAGGACAACATCATTCAGAGATCC	199		
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DB	200	TTGTAGTAACCTGCCAGCTGTGATCTTGTGATTAATACAGGAATTCAGATTTCAGATCC	259		
QY	181	ctgtcctcctaagtcttcctcagagcagtggaagaagacctgtgcatatgtaggca	240		
DB	260	CTGTCTCTCAATATGTTTCTCCAGCGAGGTGGAAGAGACCTGTGACATATGACAGCA	319		
QY	241	gtgtaaagtgctttcagagcaggaagagtgctctccaccacagcaatgcagagtgta	300		
DB	320	GTTGTAAGGTGTTTTCAGGACGACGAGAGAGTGTCTCCACCAATATGCAAGTGTGA	379		
QY	301	ctgcaactcagagtgctcactcgtcgtgggagagatgacagatgtgtgaaacagatgttaa	360		

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 QY 361 acaaggtcaagaactgcacaaagaagtgttaagaactgtgtgttttgagcatttaacga 420
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 QY 421 tcgaagaactgtgactgtgtgaccccttgacaaactgttcttgatgagaagactgtgtc 480
 Db 500 TCAGAAACGTCGACTGTGTGACCTGTGACAACTGTTCTTGGATGGAAGTCTGTGCT 559
 QY 481 tctgaatggga 491
 Db 560 TGTGAATGGGA 570
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 LOCUS 139153 MARC 1P1G Sus scrofa cDNA 5', mRNA sequence.
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 ACCESSION BE233113.1 GI:9017831
 VERSION BE233113.1
 KEYWORDS EST.
 SOURCE pig.
 ORGANISM Sus scrofa
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
 1 (bases 1 to 548)
 Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,
 Stone,R.T., Heaton,M.P., Grose,W.M., Bennett,G.A., Laegreid,W.W.
 and Keele,J.W.
 Design and use of two pooled tissue normalized cDNA libraries for
 EST discovery in swine
 Unpublished (2000)
 Contact: Smith TPL
 USDA, ARS, US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68933-0166, USA
 Tel: 402 762 4366
 Fax: 402 762 4390
 Email: smith@email.marc.usda.gov
 Single pass sequencing. Bases called and alt-trimmed with phred
 v0.980904.e. Vector identified by cross_match with the -mismatch 18
 and -mismatch 12 options.
 PCR Primers
 FORWARD: AGGAACAGCTATGACCAT
 BACKWARD: GTTTCCTCCAGTCACGACG
 Plate: 75 row: P column: 5
 Seq primer: ATTAGGTGACACTATAG.
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 Db 476 GCGAGGTGTGAACATCATCGGAATCCAGAGAGATG 513
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 LOCUS mp10f11.r1 Life Tech mouse embryo 8 5dpc 10664019 Mus musculus cDNA
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 ACCESSION AA109726
 VERSION AA109726.1 GI:1661789
 KEYWORDS EST.
 SOURCE Mus musculus.
 ORGANISM Mus musculus
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 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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 Maria,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
 Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
 Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
 Theisinger,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
 Waterston,R.
 The WashU-HMI Mouse EST Project
 Unpublished (1996)
 Contact: Maria M/Mouse EST Project
 WashU-HMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
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 /lab_host="DH10B"
 /note="Organ: whole embryo; Vector: PCMV-SPORT2; Site_1:

BASE COUNT	ORIGIN	SalI; Site-2; NotI; Cloned unidirectionally. Primer Oligo dT. 8-5dpc embryos. pCMV-SPORT2 vector."
139 a	146 c	175 g 150 t

The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
Tel: (301)-838-3529
Fax: (301)-838-0208

Query Match	28.8%	Score 241;	DB 1;	Length 610;
Best Local Similarity	67.7%	Pred. No. 2.9e-60;		
Matches 369;	Conservative 0;	Mismatches 170;	Indels 6;	Gaps 2

QY	13	taagttcaactcgtgccaagattcatcaatgggaaacagcgtttaacaatagtagcaac	72
Db	55	TGGTCTCCTGTGCATGTGCATTTTGGCCATGGGAAACACTGTTACAAAGCTGGTGCAT	114
QY	73	tctgtgtcgtgtcctcaactttagagagacaagaatcatcttcagagatccttgtagtaacy	132
Db	115	TGTGCTGGTGGCTAGTGGGGCTGTGAGAAAGTGGGAGCGCGTGCAGAACTCCTGTGTATAC	174
QY	133	cccaagctggtatcatctcgtgataataaacaagaaatcagatttgagtcctgtcctcaaa	192
Db	175	TCAGCCTGGTACTTCTCTGCAGAAATATC--AATCCAGTCTGCAGAGCTGGCCCTTCAAG	231
QY	193	tagttctcccaagcagagttgagacaagaagccgtgtgacatatacagtcagtgtaaaagtg	252
Db	232	TACCTTCTCCACATAGAGTGAGACCGCAAGCTGTATCACTTCACAGTGTGTGCACGGCTA	291
QY	253	tttcaagaccaaaggaagagtgctctccaccagaatgtcagagtgtagctcaactcagag	312
Db	292	TTTCAAGGTTCAAGAGTTTTCCTCCTACCCACAACGGGAGTGTGATGTCATTGAAG	351
QY	313	gtttcaatgctctggggccaagatgcagcatgtgtgaacaggaattgttaacaagttcaaga	372
Db	352	ATTTCATTGGCTTGGGGCCACAGTGCACCGAGAGTGTAAAGAGACTGCAGCGCTGGCCAGGA	411
QY	373	actgacaaaanaaggtttaagaactgtgtgtcttggagacattaaagatcaagaagc----	429
Db	412	GCTTAACGAAGCAGGGGTTTGCATAAACCCTGTATGCTTTGGAAATTTAATGACCAAGAACGGTAC	471
QY	430	tggcaatcgtcgaacctgagacaactgttcttcttgatgagaaagctcgtctgtgatatg	489
Db	472	TGGCGTCTGTGCACCTGGACGACACTGCTCTGTAGACGGAAGTGTGTCTTAAGACCGG	531
QY	490	gaagaagaagaggaacgtgtgtctgtgaccatctccagctgaactctcccggaagcaco	549
Db	532	GACCAACGGAAGAAGAGCTGTGTGTGTGACCGCCTGTGTAGCTTTCTCCAGTACACCACTAT	591
QY	550	ctcttg 554	
Db	592	ctgtg 596	

FEATURES	SOURCE	location/Qualifiers
	1.687	/organism="Rattus sp." /db_xref="ATCC (Inhost):2042770" /db_xref="taxon:10118" /clone="ROVDB21" /clone_1b="Normalized rat ovary. Bento Soares" /note="Organ: ovary; Vector: pT7m3pac; Site_1: EcoRI Site_2: NotI"
BASE COUNT	149 a 189 c 180 g 169 t	
ORIGIN		

Query Match	28.1%;	Score 235.2;	DB 9;	Length 687;
Best Local Similarity	67.6%;	Pred. No. 1.5e-58;		
Matches 346;	Conservative 0;	Mismatches 163;	Indels 3;	Gaps 1

QY	294	agagtgatctgcaccccaagggtttcaacttcctcgggggacagatgcagcagatglttgaaacg	353
Db	687	AGTGTAACTGCTCGTGAAGGAGATTCCTGCTTTGGGGCCAAGTGTACCAAGTGTGAGAAG	628
QY	354	attgttaaaccaagtgtaagaagactgcagcaaaaaaaggtgtgtaagaactglttcgttggacat	413
Db	627	ACTGCAAGGCCCGCCAGGAACTTAACGGAGACAGGTTGTAAAAACTGTGGCTTGGGAAGCT	568
QY	414	ttaacgactcagaacg---tggcatctgtcgaccctgcagaaactglttcgttgaatgtaa	470
Db	567	TTAAATGACACAGACGCGCCGCGCTGTCCGCGACCCCTGGAGCAACTGCTCTATGACGGAA	508
QY	471	agtcgtgctgttgtaatgtagaagagagagagaaagtgctgtgtgacatctccagctg	530
Db	507	GGTCTGTGCTTTAAGATAGGAGACCAAGGAAAGACGTGTGTGTGTGACCCCTGTGTCTA	448
QY	531	acctctctccggagagcatccctctggaaccgcgcgcgcctgcgagagagcagagacact	590
Db	447	GCCTTCTTCCCAAGTACCCACTCTTAACTGCTGTACTACTTCCAGAGAGAGATACGAGAGAC	388
QY	591	ctccgcagatcatctccctcttctctgctgctgacgctgcagatcggtgtcccttccctgctg	650
Db	387	GCCCCCTGCAGGTTCTTAACCTGTTCCGTGCGGCGCTACATTAACGGCTGCTCTGTCTCTA	328
QY	651	tctctctcaagctccggttctctctgttgtttaaacygggcagaaagaactcctgtatata	710
Db	327	TCTTTCATCATTTCTGTTCTCTGTGCCCAATATGCTCTCAGGAAGTAAGTCCCCCAACATAT	268
QY	711	tcaaacaccatttatatgtagaccagtaacaaactctccaagaaggaatgtgcttgaatgtcc	770
Db	267	TCAACCAACCAATTTAAGAGAGCGCGTTAGAACGCTCAAGAGGAAGATGCTTGTATGCTGCC	208
QY	771	gatttcagaagaagaagaagaagatgtgaa	802
Db	207	GGTTTCCAGAGGAAGAGAGAGAGAGGAGGA	176

[illegible]

RESULT	5		
AA946462/c			
LOCUS	AA946462	674 bp	mRNA
DEFINITION	EST201961	Normalized rat ovary,	Bento Soares
	ROYAR42.3,	end, mRNA sequence.	Rattus sp. cDNA clone
ACCESSION	AA946462		
VERSION	AA946462.1	GI:3106378	
KEYWORDS	EST.		
SOURCE	Rattus sp.		
ORGANISM	Rattus sp.		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;		
	Rattus.		

REFERENCE	1 (bases 1 to 674)
AUTHORS	Lee,N.H., Glodet,A., Chandra,I., Mason,T.M., Quackenbush,J.,
TITLE	Kelivavage,A.R. and Adams,M.D.
JOURNAL	Rat Genome Project: Generation of a Rat EST (RESt) Catalog & Rat
COMMENT	Gene Index Unpublished (1998) Contact: Lee, NH ATCC
FEATURES	The Institute for Genomic Research 9712, Medical Center Drive, Rockville, MD 20850, USA Tel: (301)-838-3529 Fax: (301)-838-0208 Email: nhlee@tigr.org Seq primer: M13-21. Location/Qualifiers 1. 674 /organism="Rattus sp." /db_xref="ATCC (inhost):201990" /db_xref="taxon:10118" /clone="ROVAR42" /clone_1fb="Normalized rat ovary, Bento Soares" /note="Organ: ovary; Vector: pUT3pac; Site_1: EcoRI; Site_2: NotI"
BASE COUNT	145 a 182 c 179 g 168 t
ORIGIN	
Query Match	27.6%; Score 231; DB 7; Length 674;
Best Local Similarity	68.1%; Pred. No. 2,7e-57;
Matches 337; Conservative	0; Mismatches 155; Indels 3; Gaps 1
OY	311 ggggttcacgtcctggggagagatgcagatcgtgtgtgaacagagattgtlaaacaagttcaa 370
DB	670 GGATTCACACTGCTTGGGGCCAAAGTGTACACAGTGTGAAGACGAGCTGCGCCGCCAG 611
OY	371 gaactgcacaaaaaagtggttaagaactggtcctttggacatttaagatcaagaag- 429
DB	610 GAACCTAACGGACACAGGTTGTAAAAACTGTGGGAACTTTAATACCAAGAACGCG 551
OY	430 --ttggcatctgtcgagccctggagacaactgtctcttggatgagaagtctgtgttgaat 487
DB	550 GCCGGCTGTGCGCCGACCTTGAGCAACTGCTCTTGAAGGAGGACTGTGCTTAAGAT 491
OY	488 gggagcaagagagagagagctgtgtctgtgacatctccagctgcacatctctccggagga 547
DB	490 GGGACCAAGAGAAAGACGTGTGTGTGAGACCCCTGTGTGAGCTCTCTCCAGTACC 431
OY	548 tccctgtgaccccgctgccttcgcgagagagcaagaactctccgagatcatctcc 607
DB	430 ACTCTTACTGTGTACTACTACCAAGAGAGATCAGACGAGACGCCCTTGAGGTTCT 371
OY	608 tctctctgcgctgacgtgcagctgctgtgtccttcctcgtctgtcttccagctccgt 667
DB	370 ACCTTGTTCTTGGCCCTGACATTAGCGCTGCTCTCTTCTTCTATCTTCTTCTGG 311
OY	668 tctctctgtttaaacygggcagaaagaactcctgtatatacttcaaaacacattatg 727
DB	310 TTCTCTGTGCCCCAATATGGCTCAGGAAGAGTTCCGCCACATATTTCAGCAACCATTTAAG 251
OY	728 agaccagtaacaactcactcaagaagagaagatggtctgtagctgcgattccagaagaaga 787
DB	250 AAGGGGTTAGAACGTCAACAGAGAGATGCTTGTAGCTGCCGGTTTCCAGAGAGAA 191
OY	788 gaagagagatgtgaa 802
DB	190 GAGAGAGAGAGAGGA 176
RESULT	6
LOCUS	AA087107 589 bp mRNA EST 23-OCT-1996
DEFINITION	mol3g01.r1 Life Tech mouse embryo 10 5dpc 10665016 Mus musculus
	CDNA clone IMAGE:553488 5' similar to gb:J04492 Mouse T-cell

Accession	Version	Keywords	Source	Organism	Reference	Authors	Title	Journal	Comment
receptor 4-13B	protein mRNA, complete cds (mouse);	mRNA sequence.							
AA087107	GI:1630565								
AA087107.1	GI:1630565								
EST.									
house mouse.									
house mouse.									
Mus musculus									
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.									
(bases 1 to 589)									
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,									
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,									
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,									
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and									
Waterston,R.									
The WashU-HMHI Mouse EST Project									
Unpublished (1996)									
Contact: Marra M/Mouse EST Project									
WashU-HMHI Mouse EST Project									
Washington University School of Medicine									
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108									
Tel: 314 286 1800									
Fax: 314 286 1810									
Email: mouseest@wustl.edu									
This clone is available royalty-free through LNL : contact the									
IMAGE Consortium (info@image.llnl.gov) for further information.									
GI:334280									
Seq primer: -28M13 rev1 from Amesham									
High quality sequence stop: 377.									
location/Qualifiers									
1..589									
/organism="Mus musculus"									
/strain="C57BL/6J"									
/db_xref="taxon:10090"									
/clone="IMAGE:553488"									
/clone_lib="Life Tech mouse embryo 10 5dpc 10665016"									
/library_type="embryo"									
/div_stage="10.5dpc embryos"									
/lab_host="DH10B"									
/note="Organ: whole embryo; Vector: pCMV-SPORT2; Site_1:									
SalI; Site_2: NotI; Cloned unidirectionally. Primer:									
0150 dF. 10.5dpc embryos. pCMV-SPORT2 vector."									
BASE COUNT	133 a	138 c	171 g	147 t					
ORIGIN									
Query Match	24.2%	Score 203.2:	DB 1:	Length 589:					
Best Local Similarity	67.6%	Pred. No. 4.1e-49:							
Matches 345; Conservative 0; Mismatches 158; Indels 7; Gaps 4.									
13	tagatcatacgtgacagatcattcatcatcttgaggaaacagctgttacaatagtagccac	72							
56	TGGTCTCTCTGTCACATGTCACATTTGGCCATGSGAACAACATCTTACMAAGTGTGTCTAT	115							
73	tctgttctgtgctcctcaacttgagaggaacaagatcatctgcaagatccttgaagtaactg	132							
116	TGTGCTGCTGTGACAGGGCTGTGAAGAAGTGGAGCCGTCGAGAACTCCTGTGATTAACGTG	175							
133	ccacagctggtacatctctgtataataaagaagatcagatttcagtcctgtccctccaaa	192							
176	TCAGCTGTGACTTCTCTGCAAAAATAC--AATCCAGTCTGCAAGAGCTGCCCTCCAAAG	232							
193	tagttctccacgacgagtgagacaagaacagctgtacatatcaagcagtgtaaagtgct	252							
233	TACCTCTCCACGACATAGGTGAGACACCCGACACCTGTAACTCTGCAGAGTGTGCGACGCTA	292							
253	tttcaagacgaaggaagtgcttctcaccacgaacgaatgcagagtgtagctgcatccag	312							
293	TTTCAAGTTCGAAGAAGTTTGTCTCTTAACCCACCAACGCGAGGTGTGATGATGAAGG	352							
313	gtttcattcgtctgggggcaagatgtgatactgtgttaacaaggaattgaaacaagtcgaag	372							
353	ATTCATTGCTTGGGGCCACAGTGCACCAAGATGTGAAGAGGACCTCAGGCCCTGGACAGCA	412							

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OY 373 a-cgcagcaaaaaaggtgtgtataagactgttctgttggaacttaacagataagaacg-- 429
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 413 AGCTACGAAACAGGCTTGCAAAACCTGTACCTGGGAACTTTAATGACAGAAAGGGA 472
OY 430 tggatctgtgcaccctggacaacactgttcttgatggaagtcgtgcttggaatgg 489
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 473 GGTGTTCTGTGACCTTGCGGAGGTGCGCTCTATTCTTATGCTGTGC-TAAGACCGG 531
OY 490 gacgaagagagagagcgtgtgtcttgacc 519
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 532 GACCACGAGAGAGACGCTGTGTGAGAC 561

RESULT 7
LOCUS A1664286 491 bp mRNA EST 10-MAY-1999
DEFINITION ue83h05.r1 Soares NMPu Mus musculus cDNA clone IMAGE:149753 5',
similar to gb:J04492 Mouse T-cell receptor 4-1BB protein mRNA,
complete cds (MOUSE);, mRNA sequence.
VERSION A1664286
KEYWORDS A1664286.1 GI:4767869
SOURCE EST.
ORGANISM house mouse.
MUS musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE 1 (bases 1 to 491)
AUTHORS NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
MGI:935357
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 419.
Location/Qualifiers
1. 491
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:149753"
/clone_1id="Soares_NMPu"
/sex="female"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: uterus; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; 1st strand cDNA was prepared from
pregnant mouse uterus, and was then primed with a Not I -
oligo(dT) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pT7T3
vector. Library is normalized. Library was constructed by
Bento Soares and M. Fatima Bonaldo."
BASE COUNT 114 a 118 c 135 g 124 t
ORIGIN

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Db 161 TCAGCTGCTACTTCTCTCAGAAAATAC---ATCCAGCTGCAGAGCTGCCCTCCAG 217
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 193 tagttctccagcgaggttggaacaagacctgtacatgcaagcagctgaaagtgct 252
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 218 TACCTCTTCACGATAGGTGGACACCCGAACTGTACATGCAAGATGTGCGACGCTA 277
OY 253 ttccagaccaggaagagtgctccaccagcaatgcagagltgtactcactccagg 312
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 278 TTTCAAGTTCAAGAAAGTTTGCTCTTACCCACAGACCGGAGTGTGATTTGAAGG 337
OY 313 gtccatcgtcctggggcagagatgcagcatgtgtgaacagagattgtaaacagtgtaaga 372
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 338 ATTCATTGCTTGGGGCCACAGTGCACCGACGATGTGAAGAAAGACTGCAGGCTGCAGAGA 397
OY 373 actgcaaaaaaggtgtgaagactgttctgttggaacttaacagatcagaacg--- 429
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 398 GCTACGAAAGCAGGTTGCCAAAACCTGTAGCTGGGAACATTTAATGACCAAGACGATAC 457
OY 430 tggcatctgcagccctggacaacactgtctt 462
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 458 TGGCCTGTGTGACCTTGACCGACGAGCTGCTCT 490

RESULT 8
LOCUS A1172529/c 332 bp mRNA EST 05-JUL-1999
DEFINITION UT-R-C2p-nu-g-01-0-UI.s1 UT-R-C2p Rattus norvegicus cDNA clone
UT-R-C2p-nu-g-01-0-UI 3', mRNA sequence.
VERSION A1172529
KEYWORDS A1172529.1 GI:3712569
SOURCE EST.
ORGANISM Norway rat.
Rattus norvegicus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 332)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 9704447
COMMENT Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: mssoares@blue.weeg.iowa.edu
The sequence tag present in the cDNA between the NotI site and the
oligo-dr track served to identify it as a clone from the normalized
adult ovary library. cDNA library preparation: M. Fatima Bonaldo,
Ph.D. Clone distribution: clones will be available through Research
Genetics This clone is also available through the I.M.A.G.E.
Consortium at LNL (info@image.lnl.gov). IMAGE ID=178664 The
following repetitive elements were found in this cDNA sequence:
1-37, >AT_rich#low_complexity
Seq primer: M13 Forward
POLYA-No.
FEATURES
source
Location/Qualifiers
1. 332
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-C2p-nu-g-01-0-UI"
/clone_1id="UI-R-C2p"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker. Site_1: Not I; Site_2: Eco RI; The UI-R-C2p
library is a subtracted library derived from the UI-R-C1
library, which is a subtracted library derived from the

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/organism="Rattus norvegicus"  
/db_xref="taxon:10116"
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1. .291

1. .291

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/organism="Rattus norvegicus"  
/strain="Sprague-Dawley"
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/db_xref="taxon:10116"
/collection="IT-P-C20-as-d-01-0-IT"

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/clone_11b="UI-R-C2p"
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/dev_stage="adult"  
/lab_host="DH10B (Life Techno
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/note= "Vector: pT7T3D-Pac (Pharmacia LKB)
polylinker: Site 1: Not I; Site 2: XbaI; Site 3: SalI; Site 4: PstI; Site 5: KpnI; Site 6: SmaI; Site 7: BamHI; Site 8: EcoRI; Site 9: HindIII; Site 10: ClaI; Site 11: XhoI; Site 12: SpeI; Site 13: BclII; Site 14: MspI; Site 15: AclI; Site 16: HpaII; Site 17: KpnI; Site 18: SmaI; Site 19: BamHI; Site 20: EcoRI; Site 21: HindIII; Site 22: ClaI; Site 23: XhoI; Site 24: SpeI; Site 25: BclII; Site 26: MspI; Site 27: AclI; Site 28: HpaII; Site 29: KpnI; Site 30: SmaI; Site 31: BamHI; Site 32: EcoRI; Site 33: HindIII; Site 34: ClaI; Site 35: XhoI; Site 36: SpeI; Site 37: BclII; Site 38: MspI; Site 39: AclI; Site 40: HpaII; Site 41: KpnI; Site 42: SmaI; Site 43: BamHI; Site 44: EcoRI; Site 45: HindIII; Site 46: ClaI; Site 47: XhoI; Site 48: SpeI; Site 49: BclII; Site 50: MspI; Site 51: AclI; Site 52: HpaII; Site 53: KpnI; Site 54: SmaI; Site 55: BamHI; Site 56: EcoRI; Site 57: HindIII; Site 58: ClaI; Site 59: XhoI; Site 60: SpeI; Site 61: BclII; Site 62: MspI; Site 63: AclI; Site 64: HpaII; Site 65: KpnI; Site 66: SmaI; Site 67: BamHI; Site 68: EcoRI; Site 69: HindIII; Site 70: ClaI; Site 71: XhoI; Site 72: SpeI; Site 73: BclII; Site 74: MspI; Site 75: AclI; Site 76: HpaII; Site 77: KpnI; Site 78: SmaI; Site 79: BamHI; Site 80: EcoRI; Site 81: HindIII; Site 82: ClaI; Site 83: XhoI; Site 84: SpeI; Site 85: BclII; Site 86: MspI; Site 87: AclI; Site 88: HpaII; Site 89: KpnI; Site 90: SmaI; Site 91: BamHI; Site 92: EcoRI; Site 93: HindIII; Site 94: ClaI; Site 95: XhoI; Site 96: SpeI; Site 97: BclII; Site 98: MspI; Site 99: AclI; Site 100: HpaII; Site 101: KpnI; Site 102: SmaI; Site 103: BamHI; Site 104: EcoRI; Site 105: HindIII; Site 106: ClaI; Site 107: XhoI; Site 108: SpeI; Site 109: BclII; Site 110: MspI; Site 111: AclI; Site 112: HpaII; Site 113: KpnI; Site 114: SmaI; Site 115: BamHI; Site 116: EcoRI; Site 117: HindIII; Site 118: ClaI; Site 119: XhoI; Site 120: SpeI; Site 121: BclII; Site 122: MspI; Site 123: AclI; Site 124: HpaII; Site 125: KpnI; Site 126: SmaI; Site 127: BamHI; Site 128: EcoRI; Site 129: HindIII; Site 130: ClaI; Site 131: XhoI; Site 132: SpeI; Site 133: BclII; Site 134: MspI; Site 135: AclI; Site 136: HpaII; Site 137: KpnI; Site 138: SmaI; Site 139: BamHI; Site 140: EcoRI; Site 141: HindIII; Site 142: ClaI; Site 143: XhoI; Site 144: SpeI; Site 145: BclII; Site 146: MspI; Site 147: AclI; Site 148: HpaII; Site 149: KpnI; Site 150: SmaI; Site 151: BamHI; Site 152: EcoRI; Site 153: HindIII; Site 154: ClaI; Site 155: XhoI; Site 156: SpeI; Site 157: BclII; Site 158: MspI; Site 159: AclI; Site 160: HpaII; Site 161: KpnI; Site 162: SmaI; Site 163: BamHI; Site 164: EcoRI; Site 165: HindIII; Site 166: ClaI; Site 167: XhoI; Site 168: SpeI; Site 169: BclII; Site 170: MspI; Site 171: AclI; Site 172: HpaII; Site 173: KpnI; Site 174: SmaI; Site 175: BamHI; Site 176: EcoRI; Site 177: HindIII; Site 178: ClaI; Site 179: XhoI; Site 180: SpeI; Site 181: BclII; Site 182: MspI; Site 183: AclI; Site 184: HpaII; Site 185: KpnI; Site 186: SmaI; Site 187: BamHI; Site 188: EcoRI; Site 189: HindIII; Site 190: ClaI; Site 191: XhoI; Site 192: SpeI; Site 193: BclII; Site 194: MspI; Site 195: AclI; Site 196: HpaII; Site 197: KpnI; Site 198: SmaI; Site 199: BamHI; Site 200: EcoRI; Site 201: HindIII; Site 202: ClaI; Site 203: XhoI; Site 204: SpeI; Site 205: BclII; Site 206: MspI; Site 207: AclI; Site 208: HpaII; Site 209: KpnI; Site 210: SmaI; Site 211: BamHI; Site 212: EcoRI; Site 213: HindIII; Site 214: ClaI; Site 215: XhoI; Site 216: SpeI; Site 217: BclII; Site 218: MspI; Site 219: AclI; Site 220: HpaII; Site 221: KpnI; Site 222: SmaI; Site 223: BamHI; Site 224: EcoRI; Site 225: HindIII; Site 226: ClaI; Site 227: XhoI; Site 228: SpeI; Site 229: BclII; Site 230: MspI; Site 231: AclI; Site 232: HpaII; Site 233: KpnI; Site 234: SmaI; Site 235: BamHI; Site 236: EcoRI; Site 237: HindIII; Site 238: ClaI; Site 239: XhoI; Site 240: SpeI; Site 241: BclII; Site 242: MspI; Site 243: AclI; Site 244: HpaII; Site 245: KpnI; Site 246: SmaI; Site 247: BamHI; Site 248: EcoRI; Site 249: HindIII; Site 250: ClaI; 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Site 434: MspI; Site 435: AclI; Site 436: HpaII
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library is a subtracted library

UI-R-C0 library. The UI-R-C0

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source
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/organisms="Homo sapiens"
/db_xref="GDB:5183340"
/db_xref="taxon:9606"
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/db_xref="taxon:9606"  
/clone_image="1118659"  
/clone_lib="NCI_CGAP_Lu1"  
/tissue_type="lung tumor"
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/lab host="SOLR (kanamycin resistant)"
/ncce="Organ: lung; Vector: Bluescript SK-; Site:1: EcoRI
Site:2: XhoI; Cloned unidirectionally. Primer: Oligo dr.
Bulk lung tumor. 5' adaptor sequence: 5' GAATTCGGCAGCAG 3
3' adaptor sequence: 5' CTCGACGTTTTTTTTTTTTTTT 3'
Average insert size: 1.1 kb."
BASE COUNT
ORIGIN
150 a 164 g 100 t
164 c 164 g 100 t

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Query Match	4.8%	Score 40.2	DB 5	Length 578
Best Local Similarity	50.8%	Pred. No. 0.55		
Matches 96	Conservative 0	Mismatches 93	Indels 0	Gaps 0

Oy 482 gtgaatggagcagaagaaagaggacgctgtctctgaccactctccagctacctcttcgcg 541
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Db 473 GTAGATGTTCCCATGTGACCAAGAAGAGTAAGGGCCCTTCTTCCCCTGCCTGCAG 414

413 CTGGCTTCACCTGGCAGTGGCTGTCTTCTCTAGAGACCCGGGCTCTCCCTCCAGTAC 354
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Dy 602 atcccttccttctcgtgcagctgactcgctgtcctctccgctgttctctccacag 661
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Db 353 TTCGTCTTGCGCCCTTCGCTTCCCCCATTTCCCTTCACAGCTCATAGCTGTCATCTCG 294

Qy	662	ctccgcttc	6/0
Db	293	gcccttgc	285

RESULT	13
N80901/c	
LOCUS	N80901
	529 bp
	mRNA
	EST
	29-MAR-1996

ACCESSION
Z007D06.S1 Soatase-related, lung, nuclear, 9w homo sapiens cDNA clone
IMAGE:301335 3' similar to PIR:S49265 S49265 BAP1 protein - human
[2] PIR:S44279 ;, mRNA sequence.
N80901

FUNCTION	NOV2011.1	01.12.2002
KEYWORDS	EST,	
SOURCE	human.	
ORGANISM	Homo sapiens	

REFERENCE
HILLIER, L., CLARK, N., DUBUQUE, T., ELLISTON, K., HAWKINS, M., HOLLANDER, J. A., METCALE, C. D., CHOLARICA, C. A., VEREDICA, E. A., MAMMALIA; EUTHERIA; PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
1 (bases 1 to 529)

TITLE	PERSONNEL
Rifkin L., Rohlfing, T., Soares, M., Tan, F., Trevasakis, E., 'R., Williamson, A., Wohlmann, P. and Wilson, R.	Waterston
The Washu-Merck EST Project	

COMMENT
Contact: Wilson RK
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
314-285-1000

Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LINT ; contact the
LINT coordinator at est@watson.wustl.edu for details.

Seq primer: m13 -40 forward
High quality sequence stop: 316.
Location/Qualifiers
1 538

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/organism="Homo sapiens"  
/db_xref="GDB:124625"  
/db_xref="taxon:9606"  
/clone="TWAGF.301335"
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/clone_lib="Soares_fetal_lung_NbHs1.9W"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/notes="Organ: lung; Vector: pT7T3D (Pharmacia) with a

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modified polylinker; site_1: Not I; site_2: Eco RI;
strand cdna was primed with a Not I - oligo(dT) primer

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[5'-TGTTACCAATCTGATGCGAGCGAGCCGCAATTTTCTTTTCTTTT-3']
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M. Fatima Bonaldo. This library was constructed
from the same fetus as the fetal heart library, Soares
fetal heart NDBH19W."

Query Match	4.7%	Score 39.8	DB 38	Length 529
Best Local Similarity	50.3%	Pred. No. 0.7		
Matches 95	Conservative 0	Mismatches 94	Indels 0	Gaps 0

QY 482 gtgaatggagcagaagagagacgctgtctgtggaccattccagctgactcttccc 541
|| ||| | ||| | ||| | ||| | ||| |
Db 468 GTAGATGTTCCCATGTGACAAAGAAGTAAAGNCCCTCTTCCTCCCCCTGCACAAG 409

QY 542 ggagcatccctctgtgaccccgctgcccctgagagagcagagacatccgcagatc 601
 ||||| - - ||||| - - ||||| - - ||| -
 Db 408 CTGGCTTCCACCTGGCAGTGCCTGTCTTCTGAGAGCCCGGCTCTCCTCCAGTAC 349

QY 602 atccctccttccttcgcgcagcgactgctgtctcttccacg 661
||| ||| | | | | | | | | | |
Db 348 TTCGTCTTGCCCTTCTGCTTCGCCCATTCCTTCCACAGCTCAATAGCTGTAICTCG 289

QY	662	ctccgcttc	670
Db	288	gcccttgc	280

RESULT	14
BB290438	
LOCUS	BB290438
	304 bp
	mRNA
EST	09-JUL-2000

DEFINITION
BB290438 Riken full-length cDNA, 2 cDNA clones from mouse embryonic fibroblast cell line B020045F23, similar to J04492 Mouse T-cell receptor 4-1BB protein mRNA, mRNA sequence.
BB290438

KEYWORDS	EST.
SOURCE	2005-01-01
ORGANISM	house mouse,
	<i>Mus musculus</i>

REFERENCE	AUTHORS	REFERENCE	AUTHORS
Mammalia, Eutheria;	Rodentia;	Sciurognathi;	Muridae; Murinae; Mus.
1 (bases 1 to 304)			
Kono, H., Aizawa, K.,	Akahira, S., Akiyama, J.,	Arakawa, T., Carninci	

Hirozane, T., Horii, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, U., Kituchi, N., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M.

Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata, Y., Shigemoto, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Tawawa, A., Takahashi, F., Tomimaga, N., Toyama, N., Suzuki, H.

TITLE	YOSHIDA, K.	YOSHIKI, A.	YOSHIDA, K.
YANO, R., YASUNISHI, A., YOKOTA, T., M., MURAMATSU, M. and HAYASHIZAKI, Y. RIKEN MOUSE ESTs (Kono, H. et al.)			

COMMENT
Contact: Yoshihide Hayashizaki
Genome Exploration Research Group, Life Science Tsukuba Center,
genome Science Laboratory
[the Institute of Physical and Chemical Research (RIKEN) Genomic

Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: +81-298-36-9013
Fax: +81-298-36-9098

Email: genome-rtc@ic.iken.go.jp,
URL: <http://genome.irc.iken.go.jp/>
Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasak

